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(12) **United States Patent**
Kwok et al.(10) **Patent No.:** US 9,303,268 B2
(45) **Date of Patent:** Apr. 5, 2016(54) **INCREASING LOW LIGHT TOLERANCE IN PLANTS**

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- (60) Provisional application No. 60/818,569, filed on Jul. 5, 2006.

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C12N 15/87 (2006.01)
C12N 15/82 (2006.01)
C07K 14/415 (2006.01)

(52) **U.S. Cl.**

CPC **C12N 15/8271** (2013.01); **C07K 14/415** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

Methods and materials for modulating (e.g., increasing or decreasing) low light tolerance in plants are disclosed. For example, nucleic acids encoding polypeptides that confer plants with tolerance to low light are disclosed as well as methods for using such nucleic acids to transform plant cells. Also disclosed are plants having increased low light tolerance and plant products produced from plants having increased low light tolerance.

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SEQ ID NO:118-CLONE-87DC22	AESHSNKCKGICLVE	AEGSQQPQSQPQ	P-----QFQP	HQPQSPPNFP	36
SEQ ID NO:112-CLONE-832857	TISTNTRNKCK	-----	-----	-----	19
SEQ ID NO:100-CLONE-1285138	MSSDRHTPTK	DPPDHPSSSSS	N-----HHHQ	P-----LPSQPPQ	53
SEQ ID NO:114-CLONE-847799	MS SD RHT PT K	DPPDHPSSSSS	N-----HHHQ	P-----LPAQPPDQ	33
SEQ ID NO:106-CLONE-1505805	MNSIOENE-----	NSI GNSNTTN	-----AMSY	S-NLPPPSST	41
SEQ ID NO:110-CLONE-828846	MDWI PQLMEG	SSAYCCVII NL	CATCGEATO	PLSSSSSPSA	50
SEQ ID NO:120-CLONE-1025179	MDWI I CFM-G	TT NASHNT NL	-----SSSS	SSSSGSATN	44
SEQ ID NO:128-CLONE-954932	MDPI HGF M-S	TSN SHNT NL	-----TSSS	SSSSGSATN	44
SEQ ID NO:104-CLONE-1373087	MDPI HGF M-S	DPSGPSSA	-----aOPPA	-----aOPPA	27
SEQ ID NO:106-CLONE-144C417	MDSTSGGATA	PGNSNGEPCP	-----QFQP	Q-PEGSSPPA	44
SEQ ID NO:126-CLONE-604111	MASASGEAPP	POPISTEAAP	-----APPO	P----CCSSSPA	42
SEQ ID NO:146-CLONE-604111	MASASCGAPP	POPISTEAAP	-----APPO	P----CCSSSPA	42
SEQ ID NO:88-CLONE-287BC	EEADSGRSIDP	VKCDQPGPSF	-----V	-----SSPPA	27
SEQ ID NO:122-CLONE-1084747	MDISGSDRGP GP	VSEGDPGPSF	-----TP-----	-----SSPPA	28
SEQ ID NO:116-CLONE-856613	MEGETAKAA	MEGETAKAA	-----A	-----SSSS	15
SEQ ID NO:124-CLONE-1464559	MEGETAKAA	MEGETAKAA	-----A	-----SSSS	15
SEQ ID NO:118-CLONE-87DC22	RDWNTFCQYL	RNGQDPDVH S	-----	-----	66
SEQ ID NO:112-CLONE-832857	RDWNTFCQYL	MIKNPVHYW	-----	-----	69
SEQ ID NO:100-CLONE-1285138	RDWNTFCQYL	KSQNPPLMWS	-----	-----	63
SEQ ID NO:114-CLONE-847799	RDWNTFCQYL	KSQNPPLMWS	-----	-----	83
SEQ ID NO:108-CLONE-1505805	RDWNTFCQYL	KNHRPPLSLS	-----	-----	91
SEQ ID NO:110-CLONE-828846	RDWNTFCQYL	RNHRPPLSLS	-----	-----	100
SEQ ID NO:120-CLONE-1025179	RDWNTFCQYL	RNHRPPLSLS	-----	-----	94
SEQ ID NO:128-CLONE-954932	RDWNTFCQYL	RNHRPPLSLS	-----	-----	94
SEQ ID NO:104-CLONE-1373087	RDWNTFLQYL	RNHRPPLTLA	-----	-----	77
SEQ ID NO:106-CLONE-144C417	RDWNTFLQYL	KNHKPPLTLA	-----	-----	94
SEQ ID NO:126-CLONE-604111	RDWNTFLQYL	Q NHKPPLTLA	-----	-----	92
SEQ ID NO:146-CLONE-604111	RDWNTFLQYL	Q NHKPPLTLA	-----	-----	92
SEQ ID NO:88-CLONE-287BC	RPSRYESQKR	RPSRYESQKR	-----	-----	77
SEQ ID NO:122-CLONE-1084747	RPSRYESQKR	RPSRYESQKR	-----	-----	78
SEQ ID NO:116-CLONE-856613	RPSRYESQKR	RPSRYESQKR	-----	-----	65
SEQ ID NO:124-CLONE-1464559	RDWNTFLQYL	RDWNTFLQYL	-----	-----	65

Figure 1

SEQ-ID-NO-118-CLONE-870022	R NPFAGGCR	CPLKOAWGSSL	FEE-NGGLPE	135
SEQ-ID-NO-112-CLONE-832857	KVHIIHGCVFF	CQKEPPGECCN	YEE-NGGLPE	118
SEQ-ID-NO-100-CLONE-1285138	KVHIIQCCVF	CQKDPGPFCF	YEEHGGCSFD	133
SEQ-ID-NO-114-CLONE-847799	KVHIIHQACVF	CQPDPPCPCT	YEEHGGSSPD	133
SEQ-ID-NO-116-CLONE-1505805	KVHIIPICCF	CQPNPPAPCF	FEELNGGLPE	140
SEQ-ID-NO-108-CLONE-828846	KVHIIPICCFY	CQPNPPAPCA	FEELNGGLPE	149
SEQ-ID-NO-110-CLONE-828846	KVHIIPICCFY	CQPNPPAPCA	FEELNGGLPE	143
SEQ-ID-NO-120-CLONE-10225179	KVHIIPICCFY	CQPNPPAPCA	FEELNGGLPE	143
SEQ-ID-NO-128-CLONE-964932	KVHMQLCFFF	CQPNPPAPCT	YEE-SCCP	126
SEQ-ID-NO-104-CLONE-1373087	KVHASGCCFY	CQPSPPCP	YEE-SCCP	126
SEQ-ID-NO-106-CLONE-1440417	KVHTTGC5YF	CQPNPPAPCS	YEE-NGGLPE	143
SEQ-ID-NO-126-CLONE-864111	KVHTTGC5YF	CQPNPPAPCA	YEE-NGGLPE	141
SEQ-ID-NO-146-CLONE-864111	KVHTTGC5YF	CQPNPPAPCA	YEE-NGGLPE	141
SEQ-ID-NO-88-CLONE-28780	KVHYAACPYF	CQDQPPSPCS	YEE-NGGLPE	126
SEQ-ID-NO-122-CLONE-1084747	KVHYAACPYF	CQDQPPSPCA	YEE-NGGLPE	127
SEQ-ID-NO-116-CLONE-856813	KVHTTACPF	CQPNPPSCT	FEELNGGLPE	115
SEQ-ID-NO-124-CLONE-1464359	KVHYAACPYF	CQTPPPACCT	DSLIGRLRAA	115
SEQ-ID-NO-118-CLONE-870022	R NPFAGGCR	CPLKOAWGSSL	R KKKRKKR	171
SEQ-ID-NO-112-CLONE-832857	KNPFARGGSR	CPLKOAWGSSL	AKARGVYKK	154
SEQ-ID-NO-100-CLONE-1285138	FNPFANGSIR	VHLREVRESQ	AKARGIYFK	169
SEQ-ID-NO-114-CLONE-847799	TNPFAANGSI	R VHLREVRESQ	AKARGIYRK	169
SEQ-ID-NO-108-CLONE-1505805	ANPFGAARVR	YLREVRODQ	SKARGISYEK	189
SEQ-ID-NO-110-CLONE-828846	TNPFGAARVR	YLREVRODQ	SKARGVSYEK	191
SEQ-ID-NO-120-CLONE-10225179	TNPFGAARVR	YLREVRODQ	AKARGISYEK	179
SEQ-ID-NO-128-CLONE-964932	TNPFGAARVR	YLREVRODQ	AKARGIYEK	180
SEQ-ID-NO-104-CLONE-1373087	SNPFAARVR	YLREVREEQ	AKARGISQAO	176
SEQ-ID-NO-106-CLONE-1440417	SNEFGAARVR	YLREVREEQ	PAGVEPSCSS	192
SEQ-ID-NO-126-CLONE-864111	SNEFGAARVR	YLREVREEQ	AVSNASYSVK	190
SEQ-ID-NO-146-CLONE-864111	SNEFGAARVR	YLREVREEQ	TVSSGGCGSS	190
SEQ-ID-NO-88-CLONE-28780	SNFPAARVR	YLREVREEQ	AKRKRRTVY	167
SEQ-ID-NO-122-CLONE-1084747	SNFPAARVR	YLREVREEQ	AKRKRPTVT	168
SEQ-ID-NO-116-CLONE-856813	SNFPAAKVR	YLKEVROTQ	AKRKRTHIT	153
SEQ-ID-NO-124-CLONE-1464359	SNFPAAKVR	YLKEVROTQ	AKRKRTRT	153

Figure 1 (continued)

SEQ ID NO:118-CLONE:870022	-RNPWKEHDC	EPCUTGTSSS	SNLAS	195
SEQ ID NO:112-CLONE:832857	-KNEVVVVKK	V[G]CF	SII WT	164
SEQ ID NO:100-CLONE:1285138	-KNEVVVKK	DVANSSTPNO	SFT	188
SEQ ID NO:114-CLONE:847798	-KNEVVVKK	DVANSSTPNO	SFT	191
SEQ ID NO:108-CLONE:1505805	LPMPPPPARS	ADMNLLMQ	FIVVILLVMS	239
SEQ ID NO:110-CLONE:8228846	SSSSAVSHQ	QFOMLPCTSE	LAVVLWSVLG	219
SEQ ID NO:120-CLONE:1025179	-PFPLPPAQP	AISSEPN-	TRQLKFEK	219
SEQ ID NO:128-CLONE:954932	SAAAAAGGG	DA[G]CGCAA	TAPSAS	195
SEQ ID NO:104-CLONE:1373D87	AAAGGSNSGG	DA[G]CGGDS	AAATSSAAA	212
SEQ ID NO:106-CLONE:1440417	GAVASPGCC	DT[AI]CGGAGS	SASLISATA	228
SEQ ID NO:128-CLONE:604111	CAVASPSGCC	DT[AI]CCGACG	TANDTTTV	229
SEQ ID NO:146-CLONE:604111	VRDVAVASRQ	SDCDPCNVCA	TANDTTTV	229
SEQ ID NO:88-CLONE:28780	VRDVAVASRQ	SEGDCCNIGD	PSVAEA[V]PP	196
SEQ ID NO:122-CLONE:1084747	DIATPIEGSDC	DDAECSGIC	PSSLAEVAPP	198
SEQ ID NO:116-CLONE:856813	AKETQKFDGC	AEVVIATTV	-----	182
SEQ ID NO:124-CLONE:1464359	EEGAECSSGCD	SALVITSATV	-----	183
SEQ ID NO:118-CLONE:870022	-	-	-	195
SEQ ID NO:112-CLONE:832857	-	-	-	164
SEQ ID NO:100-CLONE:1285136	-	-	-	188
SEQ ID NO:114-CLONE:847798	-	-	-	191
SEQ ID NO:108-CLONE:1505805	-	-	-	240
SEQ ID NO:110-CLONE:8228846	-	-	-	219
SEQ ID NO:120-CLONE:1025179	-	-	-	195
SEQ ID NO:128-CLONE:964932	-	-	-	199
SEQ ID NO:104-CLONE:1373D87	-	-	-	212
SEQ ID NO:106-CLONE:1440417	-	-	-	228
SEQ ID NO:126-CLONE:604111	-	-	-	228
SEQ ID NO:146-CLONE:604111	-	-	-	229
SEQ ID NO:88-CLONE:28780	-	-	-	196
SEQ ID NO:122-CLONE:1084747	-	-	-	198
SEQ ID NO:116-CLONE:856813	-	-	-	182
SEQ ID NO:124-CLONE:1464359	-	-	-	183

Figure 1 (continued)

Figure 2

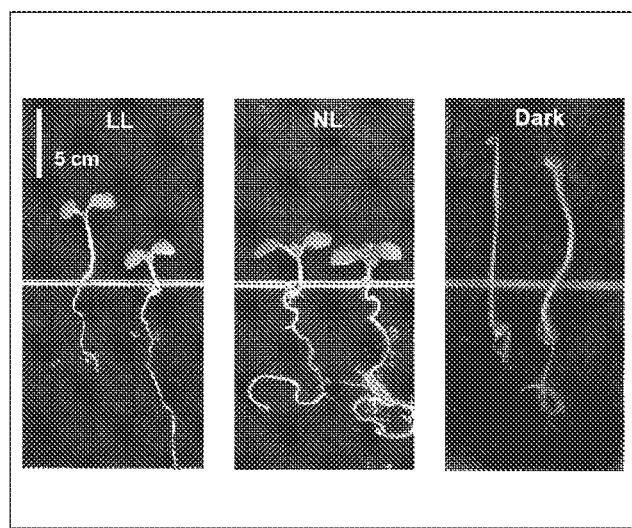


Figure 3

				S1	S2	S3	S4
				NL	NL	NL	NL
				3W	1W	1W	3W

1**INCREASING LOW LIGHT TOLERANCE IN PLANTS****CROSS-REFERENCE TO RELATED APPLICATION**

This application is a divisional of U.S. application Ser. No. 12/307,561, filed Nov. 23, 2009, now U.S. Pat. No. 8,344,210, which is a National Stage application under 35 U.S.C. §371 of International Application No. PCT/US2007/072877, having an International Filing Date of Jul. 5, 2007, which claims the benefit of priority of U.S. Provisional Application Ser. No. 60/818,569, having a filing date of Jul. 5, 2006, all of which are incorporated herein in their entirety.

TECHNICAL FIELD

This document relates to methods and materials involved in tolerance of plants to low light conditions. For example, this document provides transgenic plants and seeds comprising nucleic acids encoding polypeptides that confer tolerance to conditions of low light irradiance.

BACKGROUND

Light is the source of energy that fuels plant growth through photosynthesis. Light is also a developmental signal that modulates morphogenesis, such as de-etiolation and the transition to reproductive development. Since plants cannot choose their surroundings, they are forced to adapt their growth to ambient light conditions and have evolved complex mechanisms for monitoring the quantity and quality of the surrounding light. For example, many kinds of plants respond to growth under dense canopies or at high densities by growing faster and taller (Cerdan and Chory (2003) *Nature*, 423: 881). Densely planted crops tend to place energy into stem and petiole elongation to lift the leaves into the sunlight rather than putting energy into storage or reproductive structures. The response to low light conditions negatively affects crop yields by reducing the amount of harvestable products such as seeds, fruits and tubers. In addition, tall spindly plants tend to be less wind resistant and lodge more easily, further reducing crop yield.

There is a continuing need for plants that can thrive under less than optimal environmental conditions. One strategy to improve a plant's ability to withstand suboptimal environmental conditions relies upon traditional plant breeding methods. Another approach involves genetic manipulation of plant characteristics through the introduction of exogenous nucleic acids conferring a desirable trait.

SUMMARY

This document provides methods and materials related to low light tolerance in plants, plant cells, and seeds. For example, this document provides transgenic plants having increased tolerance to conditions of low light irradiance, nucleic acids used to generate transgenic plants having increased tolerance to low light conditions, and methods for making transgenic plants having increased tolerance to low light conditions. Transgenic plants having increased tolerance to low light conditions can exhibit a reduction in one or more responses typically elicited by low light stress. For example, a low light-tolerant transgenic plant have a hypocotyl length, when exposed to low light conditions, e.g., an irradiance of 0.01 to 20 μmol/m²/s of light, that is shorter than the typical hypocotyl length of corresponding wild-type

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plants grown under similar conditions. Increasing the tolerance of plants to low light conditions can produce healthier plants and a higher crop yield under conditions of low light irradiance, such as those occurring during high-density cultivation of plants.

In one aspect, a method of modulating the low light tolerance of a plant is provided. The method comprises introducing into a plant cell an exogenous nucleic acid comprising a nucleotide sequence encoding a polypeptide having 80% or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, and SEQ ID NO:146, where a plant produced from the plant cell exhibits a phenotypic difference relative to a corresponding control plant under low light conditions. The nucleotide sequence can encode a polypeptide comprising an amino acid sequence corresponding to SEQ ID NO:88.

In another aspect, a method of modulating the low light tolerance of a plant is provided. The method comprises introducing into a plant cell an exogenous nucleic acid comprising a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129-130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, and SEQ ID NO:143-145, where a plant produced from the plant cell exhibits a phenotypic difference relative to a corresponding control plant under low light conditions. The nucleotide sequence can comprise the nucleotide sequence set forth in SEQ ID NO:87.

The low light conditions can comprise an irradiance of about 0.01 to about 20 μmol/m²/s of light. The phenotypic difference can comprise a decreased hypocotyl length. The exogenous nucleic acid can be operably linked to a regulatory region. The regulatory region can be a tissue-preferential, broadly expressing, or inducible promoter. The plant can be a dicot. The plant can be a member of the genus *Brassica*, *Glycine*, *Gossypium*, *Helianthus*, *Lactuca*, or *Medicago*. The plant can be a monocot. The plant can be a member of the genus *Cocos*, *Elaeis*, *Oryza*, *Panicum*, or *Zea*. The method can further comprises the step of producing a plant from the plant cell. The introducing step can comprise introducing the nucleic acid into a plurality of plant cells. The method can further comprise the step of producing a plurality of plants from the plant cells. The method can further comprise the step of selecting one or more plants from the plurality of plants that have the phenotypic difference.

In another aspect, a method of producing a plant is provided. The method comprises growing a plant cell comprising an exogenous nucleic acid comprising a nucleotide sequence encoding a polypeptide having 80% or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID

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NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, and SEQ ID NO:146, where the plant exhibits a phenotypic difference relative to a corresponding control plant under low light conditions. The nucleotide sequence can encode a polypeptide comprising an amino acid sequence corresponding to SEQ ID NO:88.

In another aspect, a method of producing a plant is provided. The method comprises growing a plant cell comprising an exogenous nucleic acid comprising a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NOs: 129-130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, and SEQ ID NOs:143-145, where the plant exhibits a phenotypic difference relative to a corresponding control plant under low light conditions. The nucleotide sequence can comprise the nucleotide sequence set forth in SEQ ID NO:87.

The low light conditions can comprise an irradiance of about 0.01 to about 20 $\mu\text{mol}/\text{m}^2/\text{s}$ of light. The phenotypic difference can comprise a decreased hypocotyl length. The exogenous nucleic acid can be operably linked to a regulatory region. The regulatory region can be a tissue-preferential, broadly expressing, or inducible promoter. The plant can be a dicotyledonous plant. The plant can be a member of the genus *Brassica*, *Glycine*, *Gossypium*, *Helianthus*, *Lactuca*, or *Medicago*. The plant can be a monocotyledonous plant. The plant can be a member of the genus *Cocos*, *Elaeis*, *Oryza*, *Panicum*, or *Zea*.

In another aspect, a plant comprising an exogenous nucleic acid is provided. The exogenous nucleic acid comprises a nucleotide sequence encoding a polypeptide having 80% or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, and SEQ ID NO:146, where the plant exhibits a phenotypic difference relative to a corresponding control plant under low light conditions. The nucleotide sequence can encode a polypeptide comprising an amino acid sequence corresponding to SEQ ID NO:88.

In another aspect, a plant comprising an exogenous nucleic acid is provided. The exogenous nucleic acid comprises a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NOs:129-130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, and SEQ ID NOs:143-145, where the plant exhibits

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a phenotypic difference relative to a corresponding control plant under low light conditions. The nucleotide sequence can comprise the nucleotide sequence set forth in SEQ ID NO:87.

The low light conditions can comprise an irradiance of about 0.01 to about 20 $\mu\text{mol}/\text{m}^2/\text{s}$ of light. The phenotypic difference can comprise a decreased hypocotyl length. The exogenous nucleic acid can be operably linked to a regulatory region. The regulatory region can be a tissue-preferential, broadly expressing, or inducible promoter. The plant can be a dicot. The plant can be a member of the genus *Brassica*, *Glycine*, *Gossypium*, *Helianthus*, *Lactuca*, or *Medicago*. The plant can be a monocot. The plant can be a member of the genus *Cocos*, *Elaeis*, *Oryza*, *Panicum*, or *Zea*.

Progeny of any of the plants described above also are provided. The progeny exhibits a phenotypic difference relative to a corresponding control plant under low light conditions. Seed, vegetative tissue, and fruit from any of the plants described above also are provided, as are food products and feed products comprising seed or vegetative tissue from any of the plants described above.

In another aspect, an isolated nucleic acid molecule is provided. The isolated nucleic acid molecule comprises a nucleotide sequence having 95% or greater sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NOs:129-130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, and SEQ ID NOs:143-145.

In another aspect, an isolated nucleic acid is provided. The isolated nucleic acid molecule comprises a nucleotide sequence encoding a polypeptide having 80% or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, and SEQ ID NO:146.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although methods and materials similar or equivalent to those described herein can be used to practice the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF THE DRAWINGS

FIG. 1 is an alignment of Clone 28780 (SEQ ID NO:88) with homologous and/or orthologous amino acid sequences

Clone 1285138 (SEQ ID NO:100), Clone 1373087 (SEQ ID NO:104), Clone 1440417 (SEQ ID NO:106), Clone 1505805 (SEQ ID NO:108), Clone 828846 (SEQ ID NO:110), Clone 832857 (SEQ ID NO:112), Clone 847799 (SEQ ID NO:114), Clone 856813 (SEQ ID NO:116), Clone 870022 (SEQ ID NO:118), Clone 1025179 (SEQ ID NO:120), Clone 1084747 (SEQ ID NO:122), Clone 1464359 (SEQ ID NO:124), Clone 604111(a) (SEQ ID NO:126), Clone 964932 (SEQ ID NO:128), and Clone 604111(b) (SEQ ID NO:146).

FIG. 2 is an image of T₃ seedlings from a single insertion event of transgenic line ME05917 (right) and corresponding non-transgenic segregants (left) that were grown in the dark or under conditions of irradiation with 10 or 100 μmol/m²/s of white light (LL or NL, respectively).

FIG. 3 is a schematic diagram depicting the time course for measuring parameters of adult plants grown under normal light (NL) or low light (LL) conditions. NL and LL refer to conditions of irradiance with about 150 and 15 μmol/m²/s of light, respectively.

DETAILED DESCRIPTION

The invention features methods and materials related to modulating the tolerance of plants to conditions of low light irradiation. The methods can include transforming a plant with a nucleic acid encoding a polypeptide, the expression of which results in increased tolerance to low light conditions. Plants produced using such methods can be grown to produce seeds that, in turn, can be used to grow plants having an increased tolerance to conditions of low light irradiance.

Low light conditions can include conditions under which a plant is irradiated with about 0.01 to 20 μmol/m²/s of white light. Plants grown under low light conditions typically exhibit one or more phenotypic changes, or responses, such as an increase in extension growth. Low light tolerance refers to the ability of a plant to grow under low light irradiance levels while exhibiting a low light response that is less than the corresponding low light response exhibited by a control plant. For example, a plant that is tolerant to low light conditions can exhibit less hypocotyl elongation when exposed to low light conditions than a corresponding control plant grown under similar conditions.

Polypeptides

The term “polypeptide” as used herein refers to a compound of two or more subunit amino acids, amino acid analogs, or other peptidomimetics, regardless of post-translational modification, e.g., phosphorylation or glycosylation. The subunits may be linked by peptide bonds or other bonds such as, for example, ester or ether bonds. The term “amino acid” refers to natural and/or unnatural or synthetic amino acids, including D/L optical isomers. Full-length proteins, analogs, mutants, and fragments thereof are encompassed by this definition.

Polypeptides described herein include low light-tolerance polypeptides that, when expressed in a plant, can modulate the tolerance of the plant to conditions of low light irradiation. Modulation of the level of low light tolerance can be either an increase or a decrease in the level of low light tolerance relative to the corresponding level in a control plant.

A low light-tolerance polypeptide can contain a DUF640 domain, which is a conserved region found in a family of plant polypeptides including the resistance protein-like polypeptide. SEQ ID NO:88 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres Clone 28780 (SEQ ID NO:87), that is predicted to encode a polypeptide containing a DUF640 domain. A low light-tolerance polypeptide can comprise the amino acid sequence set

forth in SEQ ID NO:88. Alternatively, a low light-tolerance polypeptide can be a homolog, ortholog, or variant of the polypeptide having the amino acid sequence set forth in SEQ ID NO:88. For example, a low light-tolerance polypeptide can have an amino acid sequence with greater than 63% sequence identity, e.g., 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:88.

Amino acid sequences of homologs and/or orthologs of the polypeptide having the amino acid sequence set forth in SEQ ID NO:88 are provided in FIG. 1. For example, the alignment in FIG. 1 provides the amino acid sequences of Ceres Clone 28780 (SEQ ID NO:88), Clone 1285138 (SEQ ID NO:100), Clone 1373087 (SEQ ID NO:104), Clone 1440417 (SEQ ID NO:106), Clone 1505805 (SEQ ID NO:108), Clone 828846 (SEQ ID NO:110), Clone 832857 (SEQ ID NO:112), Clone 847799 (SEQ ID NO:114), Clone 856813 (SEQ ID NO:116), Clone 870022 (SEQ ID NO:118), Clone 1025179 (SEQ ID NO:120), Clone 1084747 (SEQ ID NO:122), Clone 1464359 (SEQ ID NO:124), Clone 604111(a) (SEQ ID NO:126), Clone 964932 (SEQ ID NO:128), and Clone 604111(b) (SEQ ID NO:146). Other homologs and/or orthologs include SEQ ID NOs:89-90, SEQ ID NOs:92-94, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, and SEQ ID NOs:141-142. In some cases, a low light-tolerance polypeptide includes a polypeptide having at least 80% sequence identity, e.g., 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to an amino acid sequence corresponding to any one of SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, or SEQ ID NO:146.

A low light-tolerance polypeptide encoded by a recombinant nucleic acid can be a native low light-tolerance polypeptide, i.e., one or more additional copies of the coding sequence for a low light-tolerance polypeptide that is naturally present in the cell. Alternatively, a low light-tolerance polypeptide can be heterologous to the cell, e.g., a transgenic *Lycopersicon* plant can contain the coding sequence for a low light-tolerance polypeptide from a *Glycine* plant.

A low light-tolerance polypeptide can include additional amino acids that are not involved in modulation of low light tolerance, and thus can be longer than would otherwise be the case. For example, a low light-tolerance polypeptide can include an amino acid sequence that functions as a reporter. Such a low light-tolerance polypeptide can be a fusion protein in which a green fluorescent protein (GFP) polypeptide is fused to, e.g., SEQ ID NO:88, or in which a yellow fluorescent protein (YFP) polypeptide is fused to, e.g., SEQ ID NO:88. In some embodiments, a low light-tolerance polypeptide includes a purification tag, a chloroplast transit peptide, a mitochondrial transit peptide, or a leader sequence added to the amino or carboxy terminus.

Low light-tolerance polypeptide candidates suitable for use in the invention can be identified by analysis of nucleotide and polypeptide sequence alignments. For example, performing a query on a database of nucleotide or polypeptide sequences can identify homologs and/or orthologs of low

light-tolerance polypeptides. Sequence analysis can involve BLAST, Reciprocal BLAST, or PSI-BLAST analysis of non-redundant databases using known low light-tolerance polypeptide amino acid sequences. Those polypeptides in the database that have greater than 40% sequence identity can be identified as candidates for further evaluation for suitability as a low light-tolerance polypeptide. Amino acid sequence similarity allows for conservative amino acid substitutions, such as substitution of one hydrophobic residue for another or substitution of one polar residue for another. If desired, manual inspection of such candidates can be carried out in order to narrow the number of candidates to be further evaluated. Manual inspection can be performed by selecting those candidates that appear to have domains suspected of being present in low light-tolerance polypeptides, e.g., conserved functional domains.

The identification of conserved regions in a template or subject polypeptide can facilitate production of variants of wild type low light-tolerance polypeptides. Conserved regions can be identified by locating a region within the primary amino acid sequence of a template polypeptide that is a repeated sequence, forms some secondary structure (e.g., helices and beta sheets), establishes positively or negatively charged domains, or represents a protein motif or domain. See, e.g., the Pfam web site describing consensus sequences for a variety of protein motifs and domains at sanger.ac.uk/Pfam and genome.wustl.edu/Pfam. A description of the information included at the Pfam database is described in Sonnhammer et al., *Nucl. Acids Res.*, 26:320-322 (1998); Sonnhammer et al., *Proteins*, 28:405-420 (1997); and Bateman et al., *Nucl. Acids Res.*, 27:260-262 (1999). Amino acid residues corresponding to Pfam domains included in low light-tolerance polypeptides provided herein are set forth in the sequence listing. For example, amino acid residues 13 to 145 of the amino acid sequence set forth in SEQ ID NO:88 correspond to a DUF640 domain, as indicated in fields <222> and <223> for SEQ ID NO:88 in the sequence listing.

Conserved regions also can be determined by aligning sequences of the same or related polypeptides from closely related species. Closely related species preferably are from the same family. In some embodiments, alignment of sequences from two different species is adequate. For example, sequences from *Arabidopsis* and *Zea mays* can be used to identify one or more conserved regions.

Typically, polypeptides that exhibit at least about 40% amino acid sequence identity are useful to identify conserved regions. Conserved regions of related polypeptides can exhibit at least 45% amino acid sequence identity (e.g., at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% amino acid sequence identity). In some embodiments, a conserved region of target and template polypeptides exhibit at least 92%, 94%, 96%, 98%, or 99% amino acid sequence identity. Amino acid sequence identity can be deduced from amino acid or nucleotide sequences. In certain cases, highly conserved domains have been identified within low light-tolerance polypeptides. These conserved regions can be useful in identifying functionally similar (orthologous) low light-tolerance polypeptides.

In some instances, suitable low light-tolerance polypeptides can be synthesized on the basis of consensus functional domains and/or conserved regions in polypeptides that are homologous low light-tolerance polypeptides. Domains are groups of substantially contiguous amino acids in a polypeptide that can be used to characterize protein families and/or parts of proteins. Such domains have a "fingerprint" or "signature" that can comprise conserved (1) primary sequence, (2) secondary structure, and/or (3) three-dimensional confor-

mation. Generally, domains are correlated with specific in vitro and/or in vivo activities. A domain can have a length of from 10 amino acids to 400 amino acids, e.g., 10 to 50 amino acids, or 25 to 100 amino acids, or 35 to 65 amino acids, or 35 to 55 amino acids, or 45 to 60 amino acids, or 200 to 300 amino acids, or 300 to 400 amino acids.

Representative homologs and/or orthologs of the low light-tolerance polypeptide set forth in SEQ ID NO:88 are shown in FIG. 1. FIG. 1 represents an alignment of the amino acid sequence of the low light-tolerance polypeptide set forth in SEQ ID NO:88 with the amino acid sequences of corresponding homologs and/or orthologs. The amino acid sequences of the low light-tolerance polypeptide set forth in SEQ ID NO:88 and its corresponding homologs and/or orthologs have been aligned to identify conserved amino acids, as shown in FIG. 1. A dash in an aligned sequence represents a gap, i.e., a lack of an amino acid at that position. Identical amino acids or conserved amino acid substitutions among aligned sequences are identified by boxes. Each conserved region contains a sequence of contiguous amino acid residues.

Useful polypeptides can be constructed based on the conserved regions in FIG. 1. Such a polypeptide includes the conserved regions arranged in the order depicted in the Figure from amino-terminal end to carboxy-terminal end, and has at least 80% sequence identity to an amino acid sequence corresponding to any one of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, or SEQ ID NO:146. Such a polypeptide may also include zero, one, or more than one amino acid in positions marked by dashes. When no amino acids are present at positions marked by dashes, the length of such a polypeptide is the sum of the amino acid residues in all conserved regions. When amino acids are present at all positions marked by dashes, such a polypeptide has a length that is the sum of the amino acid residues in all conserved regions and all dashes.

Conserved regions can be identified by homologous polypeptide sequence analysis as described above. The suitability of polypeptides for use as low light-tolerance polypeptides can be evaluated by functional complementation studies.

Useful polypeptides can also be identified based on the polypeptides set forth in FIG. 1 using algorithms designated as Hidden Markov Models. A "Hidden Markov Model (HMM)" is a statistical model of a consensus sequence for a group of homologous and/or orthologous polypeptides. See, Durbin et al., *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids*, Cambridge University Press, Cambridge, UK (1998). An HMM is generated by the program HMMER 2.3.2 using the multiple sequence alignment of the group of homologous and/or orthologous sequences as input and the default program parameters. The multiple sequence alignment is generated by ProbCons (Do et al., *Genome Res.*, 15(2):330-40 (2005)) version 1.11 using a set of default parameters: -c, —consistency REPS of 2; -ir, —iterative-refinement REPS of 100; -pre, —pre-training REPS of 0. ProbCons is a public domain software program provided by Stanford University.

The default parameters for building an HMM (hmmbuild) are as follows: the default "architecture prior" (archpri) used

by MAP architecture construction is 0.85, and the default cutoff threshold (idlevel) used to determine the effective sequence number is 0.62. The HMMER 2.3.2 package was released Oct. 3, 2003 under a GNU general public license, and is available from various sources on the World Wide Web such as hmmer.janelia.org, hmmer.wustl.edu, and fr.com/hmmer232/. Hmmbuild outputs the model as a text file.

The HMM for a group of homologous and/or orthologous polypeptides can be used to determine the likelihood that a subject polypeptide sequence is a better fit to that particular HMM than to a null HMM generated using a group of sequences that are not homologous and/or orthologous. The likelihood that a subject polypeptide sequence is a better fit to an HMM than to a null HMM is indicated by the HMM bit score, a number generated when the subject sequence is fitted to the HMM profile using the HMMER hmmsearch program. The following default parameters are used when running hmmsearch: the default E-value cutoff (E) is 10.0, the default bit score cutoff (T) is negative infinity, the default number of sequences in a database (Z) is the real number of sequences in the database, the default E-value cutoff for the per-domain ranked hit list (domE) is infinity, and the default bit score cutoff for the per-domain ranked hit list (domT) is negative infinity. A high HMM bit score indicates a greater likelihood that the subject sequence carries out one or more of the biochemical or physiological function(s) of the polypeptides used to generate the HMM. A high HMM bit score is at least 400, and often is higher.

A low light-tolerance polypeptide can fit an HMM provided herein with an HMM bit score greater than 400 (e.g., greater than 401, 405, 410, 415, 420, 425, 430, 435, 440, 445, 450, 460, 470, 480, 490, or 500). In some cases, a low light-tolerance polypeptide can fit an HMM provided herein with an HMM bit score that is about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the HMM bit score of any homologous and/or orthologous polypeptide provided in Table 34, so long as the low-light tolerance polypeptide is not SEQ ID NO:102.

Nucleic Acids

The terms "nucleic acid" and "polynucleotide" are used interchangeably herein, and refer to both RNA and DNA, including cDNA, genomic DNA, synthetic DNA, and DNA (or RNA) containing nucleic acid analogs. Polynucleotides can have any three-dimensional structure. A nucleic acid can be double-stranded or single-stranded (i.e., a sense strand or an antisense strand). Non-limiting examples of polynucleotides include genes, gene fragments, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, siRNA, micro-RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers, as well as nucleic acid analogs.

An "isolated" nucleic acid can be, for example, a naturally-occurring DNA molecule, provided one of the nucleic acid sequences normally found immediately flanking that DNA molecule in a naturally-occurring genome is removed or absent. Thus, an isolated nucleic acid includes, without limitation, a DNA molecule that exists as a separate molecule, independent of other sequences (e.g., a chemically synthesized nucleic acid, or a cDNA or genomic DNA fragment produced by the polymerase chain reaction (PCR) or restriction endonuclease treatment). An isolated nucleic acid also refers to a DNA molecule that is incorporated into a vector, an autonomously replicating plasmid, a virus, or into the genomic DNA of a prokaryote or eukaryote. In addition, an isolated nucleic acid can include an engineered nucleic acid

such as a DNA molecule that is part of a hybrid or fusion nucleic acid. A nucleic acid existing among hundreds to millions of other nucleic acids within, for example, cDNA libraries or genomic libraries, or gel slices containing a genomic DNA restriction digest, is not to be considered an isolated nucleic acid.

Isolated nucleic acid molecules can be produced by standard techniques. For example, polymerase chain reaction (PCR) techniques can be used to obtain an isolated nucleic acid containing a nucleotide sequence described herein. PCR can be used to amplify specific sequences from DNA as well as RNA, including sequences from total genomic DNA or total cellular RNA. Various PCR methods are described, for example, in *PCR Primer: A Laboratory Manual*, Dieffenbach and Dveksler, eds., Cold Spring Harbor Laboratory Press, 1995. Generally, sequence information from the ends of the region of interest or beyond is employed to design oligonucleotide primers that are identical or similar in sequence to opposite strands of the template to be amplified. Various PCR strategies also are available by which site-specific nucleotide sequence modifications can be introduced into a template nucleic acid. Isolated nucleic acids also can be chemically synthesized, either as a single nucleic acid molecule (e.g., using automated DNA synthesis in the 3' to 5' direction using phosphoramidite technology) or as a series of oligonucleotides. For example, one or more pairs of long oligonucleotides (e.g., >100 nucleotides) can be synthesized that contain the desired sequence, with each pair containing a short segment of complementarity (e.g., about 15 nucleotides) such that a duplex is formed when the oligonucleotide pair is annealed. DNA polymerase is used to extend the oligonucleotides, resulting in a single, double-stranded nucleic acid molecule per oligonucleotide pair, which then can be ligated into a vector. Isolated nucleic acids of the invention also can be obtained by mutagenesis of, e.g., a naturally occurring DNA.

As used herein, the term "percent sequence identity" refers to the degree of identity between any given query sequence and a subject sequence. A subject sequence typically has a length that is more than 80 percent, e.g., more than 82, 85, 87, 89, 90, 93, 95, 97, 99, 100, 105, 110, 115, or 120 percent, of the length of the query sequence. A query nucleic acid or amino acid sequence is aligned to one or more subject nucleic acid or amino acid sequences using the computer program ClustalW (version 1.83, default parameters), which allows alignments of nucleic acid or protein sequences to be carried out across their entire length (global alignment). Chenna et al., *Nucleic Acids Res.*, 31(13):3497-500 (2003).

ClustalW calculates the best match between a query and one or more subject sequences, and aligns them so that identities, similarities and differences can be determined. Gaps of one or more residues can be inserted into a query sequence, a subject sequence, or both, to maximize sequence alignments. For fast pairwise alignment of nucleic acid sequences, the following default parameters are used: word size: 2; window size: 4; scoring method: percentage; number of top diagonals: 4; and gap penalty: 5. For multiple alignment of nucleic acid sequences, the following parameters are used: gap opening penalty: 10.0; gap extension penalty: 5.0; and weight transitions: yes. For fast pairwise alignment of protein sequences, the following parameters are used: word size: 1; window size: 5; scoring method: percentage; number of top diagonals: 5; gap penalty: 3. For multiple alignment of protein sequences, the following parameters are used: weight matrix: blosum; gap opening penalty: 10.0; gap extension penalty: 0.05; hydrophilic gaps: on; hydrophilic residues: Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg, and Lys; residue-specific gap pen-

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alties: on. The output is a sequence alignment that reflects the relationship between sequences. ClustalW can be run, for example, at the Baylor College of Medicine Search Launcher site (searchlauncher.bcm.tmc.edu/multi-align/multi-align.html) and at the European Bioinformatics Institute site on the World Wide Web (ebi.ac.uk/clustalw).

To determine a percent identity between a query sequence and a subject sequence, ClustalW divides the number of identities in the best alignment by the number of residues compared (gap positions are excluded), and multiplies the result by 100. The output is the percent identity of the subject sequence with respect to the query sequence. It is noted that the percent identity value can be rounded to the nearest tenth. For example, 78.11, 78.12, 78.13, and 78.14 are rounded down to 78.1, while 78.15, 78.16, 78.17, 78.18, and 78.19 are rounded up to 78.2.

The term "exogenous" with respect to a nucleic acid indicates that the nucleic acid is part of a recombinant nucleic acid construct, or is not in its natural environment. For example, an exogenous nucleic acid can be a sequence from one species introduced into another species, i.e., a heterologous nucleic acid. Typically, such an exogenous nucleic acid is introduced into the other species via a recombinant nucleic acid construct. An exogenous nucleic acid can also be a sequence that is native to an organism and that has been reintroduced into cells of that organism. An exogenous nucleic acid that includes a native sequence can often be distinguished from the naturally occurring sequence by the presence of non-natural sequences linked to the exogenous nucleic acid, e.g., non-native regulatory sequences flanking a native sequence in a recombinant nucleic acid construct. In addition, stably transformed exogenous nucleic acids typically are integrated at positions other than the position where the native sequence is found. It will be appreciated that an exogenous nucleic acid may have been introduced into a progenitor and not into the cell under consideration. For example, a transgenic plant containing an exogenous nucleic acid can be the progeny of a cross between a stably transformed plant and a non-transgenic plant. Such progeny are considered to contain the exogenous nucleic acid.

Recombinant constructs are also provided herein and can be used to transform plants or plant cells in order to modulate low light tolerance. A recombinant nucleic acid construct comprises a nucleic acid encoding a low light-tolerance polypeptide as described herein, operably linked to a regulatory region suitable for expressing the low light-tolerance polypeptide in the plant or cell. Thus, a nucleic acid can comprise a coding sequence that encodes any of the low light-tolerance polypeptides as set forth in SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:142, or SEQ ID NO:146. Examples of nucleic acids encoding low light-tolerance polypeptides are set forth in SEQ ID NO:87, SEQ ID NO:91, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NOs:129-130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, and SEQ ID NOs:143-145. In some cases, a recom-

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binant nucleic acid construct can include a nucleic acid comprising less than the full-length coding sequence of a low light-tolerance polypeptide. In some cases, a recombinant nucleic acid construct can include a nucleic acid comprising a coding sequence, a gene, or a fragment of a coding sequence or gene in an antisense orientation so that the antisense strand of RNA is transcribed.

It will be appreciated that a number of nucleic acids can encode a polypeptide having a particular amino acid sequence. The degeneracy of the genetic code is well known to the art; i.e., for many amino acids, there is more than one nucleotide triplet that serves as the codon for the amino acid. For example, codons in the coding sequence for a given low light-tolerance polypeptide can be modified such that optimal expression in a particular plant species is obtained, using appropriate codon bias tables for that species.

Vectors containing nucleic acids such as those described herein also are provided. A "vector" is a replicon, such as a plasmid, phage, or cosmid, into which another DNA segment may be inserted so as to bring about the replication of the inserted segment. Generally, a vector is capable of replication when associated with the proper control elements. Suitable vector backbones include, for example, those routinely used in the art such as plasmids, viruses, artificial chromosomes, BACs, YACs, or PACs. The term "vector" includes cloning and expression vectors, as well as viral vectors and integrating vectors. An "expression vector" is a vector that includes a regulatory region. Suitable expression vectors include, without limitation, plasmids and viral vectors derived from, for example, bacteriophage, baculoviruses, and retroviruses. Numerous vectors and expression systems are commercially available from such corporations as Novagen (Madison, Wis.), Clontech (Mountain View, Calif.), Stratagene (La Jolla, Calif.), and Invitrogen/Life Technologies (Carlsbad, Calif.).

The vectors provided herein also can include, for example, origins of replication, scaffold attachment regions (SARs), and/or markers. A marker gene can confer a selectable phenotype on a plant cell. For example, a marker can confer biocide resistance, such as resistance to an antibiotic (e.g., kanamycin, G418, bleomycin, or hygromycin), or an herbicide (e.g., chlorosulfuron or phosphinothricin). In addition, an expression vector can include a tag sequence designed to facilitate manipulation or detection (e.g., purification or localization) of the expressed polypeptide. Tag sequences, such as green fluorescent protein (GFP), glutathione S-transferase (GST), polyhistidine, c-myc, hemagglutinin, or FlagTM tag (Kodak, New Haven, Conn.) sequences typically are expressed as a fusion with the encoded polypeptide. Such tags can be inserted anywhere within the polypeptide, including at either the carboxyl or amino terminus.

Regulatory Regions

The term "regulatory region" refers to nucleotide sequences that influence transcription or translation initiation and rate, and stability and/or mobility of a transcription or translation product. Regulatory regions include, without limitation, promoter sequences, enhancer sequences, response elements, protein recognition sites, inducible elements, protein binding sequences, 5' and 3' untranslated regions (UTRs), transcriptional start sites, termination sequences, polyadenylation sequences, and introns.

As used herein, the term "operably linked" refers to positioning of a regulatory region and a sequence to be transcribed in a nucleic acid so as to influence transcription or translation of such a sequence. For example, to bring a coding sequence under the control of a promoter, the translation initiation site of the translational reading frame of the polypeptide is typi-

cally positioned between one and about fifty nucleotides downstream of the promoter. A promoter can, however, be positioned as much as about 5,000 nucleotides upstream of the translation initiation site, or about 2,000 nucleotides upstream of the transcription start site. A promoter typically comprises at least a core (basal) promoter. A promoter also may include at least one control element, such as an enhancer sequence, an upstream element or an upstream activation region (UAR). For example, a suitable enhancer is a cis-regulatory element (-212 to -154) from the upstream region of the octopine synthase (ocs) gene. Fromm et al., *The Plant Cell*, 1:977-984 (1989). The choice of promoters to be included depends upon several factors, including, but not limited to, efficiency, selectability, inducibility, desired expression level, and cell- or tissue-preferential expression. It is a routine matter for one of skill in the art to modulate the expression of a coding sequence by appropriately selecting and positioning promoters and other regulatory regions relative to the coding sequence.

Some suitable promoters initiate transcription only, or predominantly, in certain cell types. For example, a promoter that is active predominantly in a reproductive tissue (e.g., fruit, ovule, pollen, pistils, female gametophyte, egg cell, central cell, nucellus, suspensor, synergid cell, flowers, embryonic tissue, embryo sac, embryo, zygote, endosperm, integument, or seed coat) can be used. Thus, as used herein a cell type- or tissue-preferential promoter is one that drives expression preferentially in the target tissue, but may also lead to some expression in other cell types or tissues as well. Methods for identifying and characterizing promoter regions in plant genomic DNA include, for example, those described in the following references: Jordano et al., *Plant Cell*, 1:855-866 (1989); Bustos et al., *Plant Cell*, 1:839-854 (1989); Green et al., *EMBO J.*, 7:4035-4044 (1988); Meier et al., *Plant Cell*, 3:309-316 (1991); and Zhang et al., *Plant Physiology*, 110: 1069-1079 (1996).

Examples of various classes of promoters are described below. Some of the promoters indicated below as well as additional promoters are described in more detail in U.S. patent application Ser. Nos. 60/505,689; 60/518,075; 60/544,771; 60/558,869; 60/583,691; 60/619,181; 60/637,140; 60/757,544; 60/776,307; 10/957,569; 11/058,689; 11/172,703; 11/208,308; 11/274,890; 60/583,609; 60/612,891; 11/097,589; 11/233,726; 11/408,791; 11/414,142; 10/950,321; PCT/US05/011105; PCT/US05/034308; and PCT/US05/23639. Nucleotide sequences of promoters are set forth in SEQ ID NOs:1-86. It will be appreciated that a promoter may meet criteria for one classification based on its activity in one plant species, and yet meet criteria for a different classification based on its activity in another plant species.

Broadly Expressing Promoters

A promoter can be said to be "broadly expressing" when it promotes transcription in many, but not necessarily all, plant tissues. For example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the shoot, shoot tip (apex), and leaves, but weakly or not at all in tissues such as roots or stems. As another example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the stem, shoot, shoot tip (apex), and leaves, but can promote transcription weakly or not at all in tissues such as reproductive tissues of flowers and developing seeds. Non-limiting examples of broadly expressing promoters that can be included in the nucleic acid constructs provided herein include the p326 (SEQ ID NO:75), YP0144 (SEQ ID NO:54), YP0190 (SEQ ID NO:58), p13879 (SEQ ID NO:74), YP0050 (SEQ ID NO:34), p32449 (SEQ ID NO:76), 21876 (SEQ ID NO:1),

YP0158 (SEQ ID NO:56), YP0214 (SEQ ID NO:60), YP0380 (SEQ ID NO:69), PT0848 (SEQ ID NO:26), and PT0633 (SEQ ID NO:7) promoters. Additional examples include the cauliflower mosaic virus (CaMV) 35S promoter, the mannopine synthase (MAS) promoter, the 1' or 2' promoters derived from T-DNA of *Agrobacterium tumefaciens*, the figwort mosaic virus 34S promoter, actin promoters such as the rice actin promoter, and ubiquitin promoters such as the maize ubiquitin-1 promoter. In some cases, the CaMV 35S promoter is excluded from the category of broadly expressing promoters.

Photosynthetic Tissue Promoters

Promoters active in photosynthetic tissue confer transcription in green tissues such as leaves and stems. Most suitable are promoters that drive expression only or predominantly in such tissues. Examples of such promoters include the ribulose-1,5-bisphosphate carboxylase (RbcS) promoters such as the RbcS promoter from eastern larch (*Larix laricina*), the pine cab6 promoter (Yamamoto et al., *Plant Cell Physiol.*, 35:773-778 (1994)), the Cab-1 promoter from wheat (Fejes et al., *Plant Mol. Biol.*, 15:921-932 (1990)), the CAB-1 promoter from spinach (Lubberstedt et al., *Plant Physiol.*, 104: 997-1006 (1994)), the cab1R promoter from rice (Luan et al., *Plant Cell*, 4:971-981 (1992)), the pyruvate orthophosphate dikinase (PPDK) promoter from corn (Matsuoka et al., *Proc. Natl. Acad. Sci. USA*, 90:9586-9590 (1993)), the tobacco LhcB1*2 promoter (Cerdan et al., *Plant Mol. Biol.*, 33:245-255 (1997)), the *Arabidopsis thaliana* SUC2 sucrose-H⁺ symporter promoter (Truernit et al., *Planta*, 196:564-570 (1995)), and thylakoid membrane protein promoters from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other photosynthetic tissue promoters include PT0535 (SEQ ID NO:3), PT0668 (SEQ ID NO:2), PT0886 (SEQ ID NO:29), YP0144 (SEQ ID NO:54), YP0380 (SEQ ID NO:69), and PT0585 (SEQ ID NO:4).

Vascular Tissue Promoters

Examples of promoters that have high or preferential activity in vascular bundles include YP0087 (SEQ ID NO:82), YP0093 (SEQ ID NO:83), YP0108 (SEQ ID NO:84), YP0022 (SEQ ID NO:80), and YP0080 (SEQ ID NO:81). Other vascular tissue-preferential promoters include the glycine-rich cell wall protein GRP 1.8 promoter (Keller and Baumgartner, *Plant Cell*, 3(10):1051-1061 (1991)), the Commelina yellow mottle virus (CoYMV) promoter (Medberry et al., *Plant Cell*, 4(2):185-192 (1992)), and the rice tungro bacilliform virus (RTBV) promoter (Dai et al., *Proc. Natl. Acad. Sci. USA*, 101(2):687-692 (2004)).

Inducible Promoters

Inducible promoters confer transcription in response to external stimuli such as chemical agents or environmental stimuli. For example, inducible promoters can confer transcription in response to hormones such as giberellic acid or ethylene, or in response to light or drought. Examples of drought-inducible promoters include YP0380 (SEQ ID NO:69), PT0848 (SEQ ID NO:26), YP0381 (SEQ ID NO:70), YP0337 (SEQ ID NO:65), PT0633 (SEQ ID NO:7), YP0374 (SEQ ID NO:67), PT0710 (SEQ ID NO:18), YP0356 (SEQ ID NO:66), YP0385 (SEQ ID NO:72), YP0396 (SEQ ID NO:73), YP0388 (SEQ ID NO:85), YP0384 (SEQ ID NO:71), PT0688 (SEQ ID NO:15), YP0286 (SEQ ID NO:64), YP0377 (SEQ ID NO:68), PD1367 (SEQ ID NO:77), PD0901 (SEQ ID NO:79), and PD0898 (SEQ ID NO:78). Examples of nitrogen-inducible promoters include PT0863 (SEQ ID NO:27), PT0829 (SEQ ID NO:23), PT0665 (SEQ ID NO:10), and PT0886 (SEQ ID NO:29). Examples of shade-inducible promoters include PR0924 (SEQ ID NO:86), and PT0678 (SEQ ID NO:13).

Basal Promoters

A basal promoter is the minimal sequence necessary for assembly of a transcription complex required for transcription initiation. Basal promoters frequently include a "TATA box" element that may be located between about 15 and about 35 nucleotides upstream from the site of transcription initiation. Basal promoters also may include a "CCAAT box" element (typically the sequence CCAAT) and/or a GGGCG sequence, which can be located between about 40 and about 200 nucleotides, typically about 60 to about 120 nucleotides, upstream from the transcription start site.

Other Promoters

Other classes of promoters include, but are not limited to, leaf-preferential, stem/shoot-preferential, callus-preferential, guard cell-preferential, such as PT0678 (SEQ ID NO:13), and senescence-preferential promoters. Promoters designated YP0086 (SEQ ID NO:35), YP0188 (SEQ ID NO:57), YP0263 (SEQ ID NO:61), PT0758 (SEQ ID NO:22), PT0743 (SEQ ID NO:21), PT0829 (SEQ ID NO:23), YP0119 (SEQ ID NO:48), and YP0096 (SEQ ID NO:38), as described in the above-referenced patent applications, may also be useful.

Other Regulatory Regions

A 5' untranslated region (UTR) can be included in nucleic acid constructs described herein. A 5' UTR is transcribed, but is not translated, and lies between the start site of the transcript and the translation initiation codon and may include the +1 nucleotide. A 3' UTR can be positioned between the translation termination codon and the end of the transcript. UTRs can have particular functions such as increasing mRNA stability or attenuating translation. Examples of 3' UTRs include, but are not limited to, polyadenylation signals and transcription termination sequences, e.g., a nopaline synthase termination sequence.

It will be understood that more than one regulatory region may be present in a recombinant polynucleotide, e.g., introns, enhancers, upstream activation regions, transcription terminators, and inducible elements. Thus, more than one regulatory region can be operably linked to the sequence of a polynucleotide encoding a low light-tolerance polypeptide.

Regulatory regions, such as promoters for endogenous genes, can be obtained by chemical synthesis or by subcloning from a genomic DNA that includes such a regulatory region. A nucleic acid comprising such a regulatory region can also include flanking sequences that contain restriction enzyme sites that facilitate subsequent manipulation.

Transgenic Plants and Plant Cells

The invention also features transgenic plant cells and plants comprising at least one recombinant nucleic acid construct described herein. A plant or plant cell can be transformed by having a construct integrated into its genome, i.e., can be stably transformed. Stably transformed cells typically retain the introduced nucleic acid with each cell division. A plant or plant cell can also be transiently transformed such that the construct is not integrated into its genome. Transiently transformed cells typically lose all or some portion of the introduced nucleic acid construct with each cell division such that the introduced nucleic acid cannot be detected in daughter cells after a sufficient number of cell divisions. Both transiently transformed and stably transformed transgenic plants and plant cells can be useful in the methods described herein.

Transgenic plant cells used in methods described herein can constitute part or all of a whole plant. Such plants can be grown in a manner suitable for the species under consideration, either in a growth chamber, a greenhouse, or in a field. Transgenic plants can be bred as desired for a particular

purpose, e.g., to introduce a recombinant nucleic acid into other lines, to transfer a recombinant nucleic acid to other species, or for further selection of other desirable traits. Alternatively, transgenic plants can be propagated vegetatively for those species amenable to such techniques. As used herein, a transgenic plant also refers to progeny of an initial transgenic plant. Progeny includes descendants of a particular plant or plant line. Progeny of an instant plant include seeds formed on F₁, F₂, F₃, F₄, F₅, F₆ and subsequent generation plants, or seeds formed on BC₁, BC₂, BC₃, and subsequent generation plants, or seeds formed on F₁BC₁, F₁BC₂, F₁BC₃, and subsequent generation plants. The designation F₁ refers to the progeny of a cross between two parents that are genetically distinct. The designations F₂, F₃, F₄, F₅ and F₆ refer to subsequent generations of self- or sib-pollinated progeny of an F₁ plant. Seeds produced by a transgenic plant can be grown and then selfed (or outcrossed and selfed) to obtain seeds homozygous for the nucleic acid construct.

Transgenic plants can be grown in suspension culture, or tissue or organ culture. For the purposes of this invention, solid and/or liquid tissue culture techniques can be used. When using solid medium, transgenic plant cells can be placed directly onto the medium or can be placed onto a filter that is then placed in contact with the medium. When using liquid medium, transgenic plant cells can be placed onto a flotation device, e.g., a porous membrane that contacts the liquid medium. Solid medium typically is made from liquid medium by adding agar. For example, a solid medium can be Murashige and Skoog (MS) medium containing agar and a suitable concentration of an auxin, e.g., 2,4-dichlorophenoxyacetic acid (2,4-D), and a suitable concentration of a cytokinin, e.g., kinetin.

When transiently transformed plant cells are used, a reporter sequence encoding a reporter polypeptide having a reporter activity can be included in the transformation procedure and an assay for reporter activity or expression can be performed at a suitable time after transformation. A suitable time for conducting the assay typically is about 1-21 days after transformation, e.g., about 1-14 days, about 1-7 days, or about 1-3 days. The use of transient assays is particularly convenient for rapid analysis in different species, or to confirm expression of a heterologous low light-tolerance polypeptide whose expression has not previously been confirmed in particular recipient cells.

Techniques for introducing nucleic acids into monocotyledonous and dicotyledonous plants are known in the art, and include, without limitation, *Agrobacterium*-mediated transformation, viral vector-mediated transformation, electroporation and particle gun transformation, e.g., U.S. Pat. Nos. 5,538,880; 5,204,253; 6,329,571 and 6,013,863. If a cell or cultured tissue is used as the recipient tissue for transformation, plants can be regenerated from transformed cultures if desired, by techniques known to those skilled in the art.

Plant Species

The polynucleotides and vectors described herein can be used to transform a number of monocotyledonous and dicotyledonous plants and plant cell systems, including dicots such as alfalfa, almond, amaranth, apple, apricot, avocado, beans (including kidney beans, lima beans, dry beans, green beans), brazil nut, broccoli, cabbage, canola, carrot, cashew, castor bean, cherry, chick peas, chicory, chocolate, clover, cocoa, coffee, cotton, cottonseed, crambe, eucalyptus, flax, fox-glove, grape, grapefruit, hazelnut, hemp, *jatropha*, jojoba, lemon, lentils, lettuce, linseed, macadamia nut, mango, melon (e.g., watermelon, cantaloupe), mustard, neem, olive, orange, peach, peanut, pear, peas, pecan, pepper, pistachio, plum, poplar, poppy, potato, pumpkin, oilseed rape, quinoa,

rapeseed (high erucic acid and canola), safflower, sesame, soaptree bark, soybean, spinach, strawberry, sugar beet, sunflower, sweet potatoes, tea, tomato, walnut, and yams, as well as monocots such as banana, barley, bluegrass, coconut, corn, date palm, fescue, field corn, garlic, millet, oat, oil palm, onion, palm kernel oil, pineapple, popcorn, rice, rye, ryegrass, sorghum, sudangrass, sugarcane, sweet corn, switchgrass, turf grasses, timothy, and wheat. Gymnosperms such as fir, pine, and spruce can also be suitable.

Thus, the methods and compositions described herein can be used with dicotyledonous plants belonging, for example, to the orders Apiales, Arecales, Aristolochiales, Asterales, Batales, Campanulales, Capparales, Caryophyllales, Casuarinales, Celastrales, Cornales, Cucurbitales, Diapensiales, Dilleniales, Dipsacales, Ebenales, Ericales, Eucomiales, Euphorbiales, Fabales, Fagales, Gentianales, Geraniales, Haloragales, Hamamelidales, Illiciales, Juglandales, Lamiales, Laurales, Lecythidales, Leitneriales, Linales, Magnoliales, Malpighiales, Malvales, Myricales, Mytales, Nymphaeales, Papaverales, Piperales, Plantaginales, Plumbaginales, Podostemales, Polemoniales, Polygalales, Polygonales, Primulales, Proteales, Rafflesiaceae, Ranunculales, Rhamnales, Rosales, Rubiales, Salicales, Santales, Sapindales, Sarraceniaceae, Scrophulariales, Solanales, Trochodendrales, Theales, Umbellales, Urticaceae, and Violales. The methods and compositions described herein also can be utilized with monocotyledonous plants such as those belonging to the orders Alismatales, Arales, Arecales, Asparagales, Bromeliales, Commelinaceae, Cyclanthales, Cyperales, Eriocaulales, Hydrocharitales, Juncales, Liliales, Najadales, Orchidales, Pandanales, Poales, Restionales, Triuridales, Typhales, Zingiberales, and with plants belonging to Gymnospermae, e.g., Cycadales, Ephedrales, Ginkgoales, Gnetales, Taxales, and Pinales.

The methods and compositions can be used over a broad range of plant species, including species from the dicot genera *Abelmoschus*, *Acer*, *Acokanthera*, *Aconitum*, *Aesculus*, *Alangium*, *Alchornea*, *Alexa*, *Alseodaphne*, *Amaranthus*, *Ammodendron*, *Anabasis*, *Anacardium*, *Andrographis*, *Angophora*, *Anisodus*, *Apium*, *Apocynum*, *Arabidopsis*, *Arachis*, *Argemone*, *Artemisia*, *Asclepias*, *Atropa*, *Azadirachta*, *Beilschmiedia*, *Berberis*, *Bertholletia*, *Beta*, *Betula*, *Bixa*, *Bleekeria*, *Borago*, *Brassica*, *Calendula*, *Camellia*, *Campotheca*, *Canarium*, *Cannabis*, *Capsicum*, *Carthamus*, *Carya*, *Catharanthus*, *Centella*, *Cephaelis*, *Chelidonium*, *Chenopodium*, *Chrysanthemum*, *Cicer*, *Cichorium*, *Cinchona*, *Cinnamomum*, *Cissampelos*, *Citrus*, *Citrullus*, *Coccinia*, *Cocos*, *Coffea*, *Cola*, *Coleus*, *Convolvulus*, *Coptis*, *Corylus*, *Corymbia*, *Crambe*, *Crotalaria*, *Croton*, *Cucumis*, *Cucurbita*, *Cuphea*, *Cytisus*, *Datura*, *Daucus*, *Dendromecon*, *Dianthus*, *Dichroa*, *Digitalis*, *Dioscorea*, *Duguetia*, *Erythroxylum*, *Eschscholzia*, *Eucalyptus*, *Euphorbia*, *Euphorbia*, *Ficus*, *Fragaria*, *Galega*, *Gelsemium*, *Glaucium*, *Glycine*, *Glycyrrhiza*, *Gossypium*, *Helianthus*, *Heliotropium*, *Hemisleya*, *Hevea*, *Hydrastis*, *Hyoscyamus*, *Jatropha*, *Juglans*, *Lactuca*, *Landolphia*, *Lavandula*, *Lens*, *Linum*, *Litsea*, *Lobelia*, *Luffa*, *Lupinus*, *Lycopersicon*, *Macadamia*, *Mahonia*, *Majoreana*, *Malus*, *Mangifera*, *Manihot*, *Meconopsis*, *Medicago*, *Menispermum*, *Mentha*, *Micropus*, *Nicotiana*, *Ocimum*, *Olea*, *Origanum*, *Papaver*, *Parthenium*, *Persea*, *Petunia*, *Phaseolus*, *Physostigma*, *Pilocarpus*, *Pistacia*, *Pisum*, *Poinsettia*, *Populus*, *Prunus*, *Psychotria*, *Pyrus*, *Quillaja*, *Rabdossia*, *Raphanus*, *Rauwolfia*, *Rhizocarya*, *Ricinus*, *Rosa*, *Rosmarinus*, *Rubus*, *Rubia*, *Salix*, *Salvia*, *Sanguinaria*, *Scopolia*, *Senecio*, *Sesamum*, *Simmondsia*, *Sinapis*, *Sinomenium*, *Solanum*, *Sophora*, *Spinacia*, *Stephania*, *Strophanthus*, *Strychnos*, *Tagetes*, *Tanacetum*, *Theobroma*, *Thymus*, *Trifolium*, *Trigonella*, *Vaccinium*, *Vicia*, *Vigna*, *Vinca*, and *Vitis*; and the monocot genera *Agrostis*, *Allium*, *Alstroemeria*, *Ananas*, *Andropogon*, *Areca*, *Arundo*, *Asparagus*, *Avena*, *Cocos*, *Colchicum*, *Convallaria*, *Curcum*, *Cynodon*, *Elaeis*, *Eragrostis*, *Erianthus*, *Festuca*, *Festulolium*, *Galanthus*, *Hemerocallis*, *Hordeum*, *Lemna*, *Lolium*, *Miscanthus*, *Musa*, *Oryza*, *Panicum*, *Pennisetum*, *Phalaris*, *Phleum*, *Phoenix*, *Poa*, *Ruscus*, *Saccharum*, *Secale*, *Sorghum*, *Spartina*, *Triticosecale*, *Triticum*, *Uoniola*, *Veratrum*, *Zea*, and *Zoysia*; and the gymnosperm genera *Abies*, *Cephalotaxus*, *Cunninghamia*, *Ephedra*, *Picea*, *Pinus*, *Pseudotsuga*, and *Taxus*.

In some embodiments, a plant can be a species selected from *Abelmoschus esculentus* (okra), *Abies* spp. (fir), *Acer* spp. (maple), *Allium cepa* (onion), *Alstroemeria* spp., *Ananas comosus* (pineapple), *Andrographis paniculata*, *Andropogon gerardii* (big bluestem), *Artemisia annua*, *Arundo donax* (giant reed), *Atropa belladonna*, *Avena sativa*, bamboo, bent-grass (*Agrostis* spp.), *Berberis* spp., *Beta vulgaris* (sugar-beet), *Bixa orellana*, *Brassica juncea*, *Brassica napus* (canola), *Brassica rapa*, *Brassica oleracea* (broccoli, cauliflower, brussels sprouts), *Calendula officinalis*, *Camellia sinensis* (tea), *Campotheca acuminata*, *Cannabis sativa*, *Capsicum annum* (hot & sweet pepper), *Carthamus tinctorius* (safflower), *Catharanthus roseus*, *Cephalotaxus* spp., *Chrysanthemum parthenium*, *Cinchona officinalis*, *Citrullus lanatus* (watermelon), *Coffea arabica* (coffee), *Colchicum autumnale*, *Coleus forskohlii*, *Cucumis melo* (melon), *Cucumis sativus* (cucumber), *Cucurbita maxima* (squash), *Cucurbita moschata* (squash), *Cynodon dactylon* (bermudagrass), *Datura stramonium*, *Dianthus caryophyllus* (carnation), *Digitalis lanata*, *Digitalis purpurea*, *Dioscorea* spp., *Elaeis guineensis* (palm), *Ephedra sinica*, *Ephedra* spp., *Erianthus* spp., *Erythroxylum coca*, *Eucalyptus* spp. (eucalyptus), *Festuca arundinacea* (tall fescue), *Fragaria ananassa* (strawberry), *Galanthus woronowii*, *Glycine max* (soybean), *Gossypium hirsutum* (cotton), *Gossypium herbaceum*, *Helianthus annuus* (sunflower), *Hevea* spp. (rubber), *Hordeum vulgare*, *Hyoscyamus* spp., *Jatropha curcas* (*Jatropha*), *Lactuca sativa* (lettuce), *Linum usitatissimum* (flax), *Lupinus albus* (lupin), *Lycopersicon esculentum* (tomato), *Lycopodium serratum* (=*Huperzia serrata*), *Lycopodium* spp., *Manihot esculenta* (cassava), *Medicago sativa* (alfalfa), *Mentha piperita* (mint), *Mentha spicata* (mint), *Miscanthus* spp., *Miscanthus giganteus* (*Miscanthus*), *Musa paradisiaca* (banana), *Nicotiana tabacum* (tobacco), *Oryza sativa* (rice), *Panicum* spp., *Panicum virgatum* (switchgrass), *Papaver somniferum* (opium poppy), *Papaver orientale*, *Parthenium argentatum* (guayule), *Pennisetum glaucum* (pearl millet), *Pennisetum purpureum* (elephant grass), *Petunia* spp. (petunia), *Phalaris arundinacea* (reed canarygrass), *Pinus* spp. (pine), *Poinsettia pulcherrima* (poinsettia), *Populus* spp., *Populus balsamifera* (poplar), *Populus tremuloides* (aspens), *Rauwolfia serpentina*, *Rauwolfia* spp., *Ricinus communis* (castor), *Rosa* spp. (rose), *Saccharum* spp. (energycane), *Salix* spp. (willow), *Sanguinaria canadensis*, *Scopolia* spp., *Secale cereale* (rye), *Solanum melongena* (eggplant), *Solanum tuberosum* (potato), *Sorghum* spp., *Sorghum alnum*, *Sorghum bicolor* (sorghum), *Sorghum halapense*, *Sorghum vulgare*, *Spartina pectinata* (prairie cordgrass), *Spinacea oleracea* (spinach), *Tanacetum parthenium*, *Taxus baccata*, *Taxus brevifolia*, *Theobroma cacao* (cocoa), *Triticale* (wheat X rye), *Triticum aestivum* (wheat), *Uniola paniculata* (oats), *Veratrum californicum*, *Vinca rosea*, *Vitis vinifera* (grape), and *Zea mays* (corn).

65 Transgenic Plant Phenotypes

A transformed cell, callus, tissue, or plant can be identified and isolated by selecting or screening the engineered plant

material for particular traits or activities, e.g., expression of a selectable marker gene or modulation of low-light tolerance. Such screening and selection methodologies are well known to those having ordinary skill in the art. In addition, physical and biochemical methods can be used to identify transformants. These include Southern analysis or PCR amplification for detection of a polynucleotide; Northern blots, S1 RNase protection, primer-extension, or RT-PCR amplification for detecting RNA transcripts; enzymatic assays for detecting enzyme or ribozyme activity of polypeptides and polynucleotides; and protein gel electrophoresis, Western blots, immunoprecipitation, and enzyme-linked immunoassays to detect polypeptides. Other techniques such as *in situ* hybridization, enzyme staining, and immunostaining also can be used to detect the presence or expression of polypeptides and/or polynucleotides. Methods for performing all of the referenced techniques are well known.

A population of transgenic plants can be screened and/or selected for those members of the population that have a desired trait or phenotype conferred by expression of the transgene. For example, a population of progeny of a single transformation event can be screened for those plants having a desired level of expression of a low light tolerance polypeptide or nucleic acid. As an alternative, a population of plants comprising independent transformation events can be screened for those plants having increased tolerance to conditions of low light irradiation. Selection and/or screening can be carried out over one or more generations, which can be useful to identify those plants that have a desired trait, such as an increased tolerance to conditions of low light irradiation. Selection and/or screening can also be carried out in more than one geographic location. In some cases, transgenic plants can be grown and selected under conditions which induce a desired phenotype or are otherwise necessary to produce a desired phenotype in a transgenic plant. In addition, selection and/or screening can be carried out during a particular developmental stage in which the phenotype is exhibited by the plant.

The phenotype of a transgenic plant can be evaluated relative to a control plant that does not express the exogenous polynucleotide of interest, such as a corresponding wild type plant, a corresponding plant that is not transgenic for the exogenous polynucleotide of interest but otherwise is of the same genetic background as the transgenic plant of interest, or a corresponding plant of the same genetic background in which expression of the polypeptide is suppressed, inhibited, or not induced (e.g., where expression is under the control of an inducible promoter). A plant can be said "not to express" a polypeptide when the plant exhibits less than 10%, e.g., less than 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.01%, or 0.001%, of the amount of polypeptide or mRNA encoding the polypeptide exhibited by the plant of interest. Expression can be evaluated using methods including, for example, RT-PCR, Northern blots, S1 RNase protection, primer extensions, Western blots, protein gel electrophoresis, immunoprecipitation, enzyme-linked immunoassays, chip assays, and mass spectrometry. It should be noted that if a polypeptide is expressed under the control of a tissue-preferential or broadly expressing promoter, expression can be evaluated in the entire plant or in a selected tissue. Similarly, if a polypeptide is expressed at a particular time, e.g., at a particular time in development or upon induction, expression can be evaluated selectively at a desired time period.

The phenotype of a transgenic plant and a corresponding control plant that either lacks the transgene or does not express the transgene can be evaluated under particular environmental conditions. For example, the phenotype of a trans-

genic plant and a corresponding control plant can be evaluated under conditions of low light irradiance. Low light conditions are conditions under which a plant is exposed to an irradiance of about 0.01 $\mu\text{mol}/\text{m}^2/\text{s}$ of light to about 20 $\mu\text{mol}/\text{m}^2/\text{s}$ of light at room temperature and about 70% relative humidity. For example, conditions under which a plant is exposed to 0.01, 1, 5, 10, 15, or 20 $\mu\text{mol}/\text{m}^2/\text{s}$ of light are low light conditions. Sources of lighting and other equipment appropriate for controlling light conditions are known to those in art.

Low light conditions typically have light of a combination of wavelengths, such as white light. White light can be supplied, e.g., by 32 watt fluorescent bulbs (Sylvania, F032/841/ECO, Danvers, Mass.), providing a red:far-red ratio of 13:1. Red wavelengths typically range from a photon irradiance of about 630 to about 700 nm. Far-red wavelengths typically range from a photon irradiance of about 700 to about 750 nm.

In some embodiments, the phenotype of a transgenic plant is assayed under low light conditions in which there is continuous low light during the light period of a light/dark cycle. Continuous low light conditions can be, for example, 16 hours of irradiance with 0.01 to 20 $\mu\text{mol}/\text{m}^2/\text{s}$ of light alternating with 8 hours of darkness. The phenotype of a transgenic plant is assayed once the plant has been exposed to continuous low light conditions during the light period of the light/dark cycle for seven days.

A transgenic plant comprising an exogenous nucleic acid encoding a low light-tolerance polypeptide can exhibit one or more of the following phenotypic differences relative to a corresponding control plant under low light conditions: decreased extension growth, e.g., decreased petiole length, decreased hypocotyl length, decreased internode spacing, and decreased leaf elongation in cereals; increased leaf development, e.g., increased leaf thickness and reduced leaf area growth; decreased apical dominance, e.g., increased branching and tillering; increased chloroplast development, e.g., increased chlorophyll synthesis and a change in the balance of the chlorophyll a:b ratio; alterations in flowering and seed/fruit production, e.g., an increased rate of flowering, an increase in seed set, and increased fruit development; and an increase in storage organ deposition.

Typically, a difference (e.g., an increase) in a morphological feature in a transgenic plant or cell relative to a control plant or cell is considered statistically significant at $p \leq 0.05$ with an appropriate parametric or non-parametric statistic, e.g., Chi-square test, Student's t-test, Mann-Whitney test, or F-test. In some embodiments, a difference in the dimensions of any individual morphological feature is statistically significant at $p < 0.01$, $p < 0.005$, or $p < 0.001$. A statistically significant difference in, for example, a morphological feature in a transgenic plant compared to the corresponding morphological feature a control plant indicates that (1) expression of the recombinant nucleic acid present in the transgenic plant confers the alteration in the morphological feature and/or (2) the recombinant nucleic acid warrants further study as a candidate for altering the morphological feature in a plant.

One suitable phenotype to measure is hypocotyl length. When wild-type seedlings are grown under low light conditions, the hypocotyl length is typically significantly increased relative to the hypocotyl length found in wild-type seedlings grown under conditions of irradiance with about 100 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light.

Seedlings of a transgenic plant and seedlings of a corresponding control plant that either lacks the transgene or does not express the transgene can be grown under low light conditions and, at the appropriate time, hypocotyl lengths from seedlings of each group can be measured. Under low light

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conditions, a seedling in which the expression of a low light-tolerance polypeptide is increased can have a significantly shorter hypocotyl length than a seedling of a corresponding control plant. The hypocotyl length can be shorter by at least 10 percent, e.g., 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, or more than 75 percent, as compared to the hypocotyl length of a corresponding control plant.

Transgenic plants provided herein have particular uses in agricultural industries. For example, transgenic plants expressing a low light-tolerance polypeptide provided herein can be superior to corresponding control plants in maintaining development and maturation under low light conditions. Such a trait can increase plant survival and seedling establishment at high plant densities, even in crops when plants are near mature growth stages. Transgenic plants expressing a low light-tolerance polypeptide can be more densely planted than those that are not tolerant to low light conditions. Expression of a low light-tolerant polypeptide in plants can provide increased yields compared to plants that are not low light tolerant and that are grown under similar conditions. In addition, expression of polypeptide conferring low light-tolerance in a plant, such as corn, can ensure reasonable seed set in the event that low light conditions prevail during critical stages of plant development, e.g., pollination.

The materials and methods described herein are useful for modifying biomass characteristics, such as characteristics of biomass renewable energy source plants. A biomass renewable energy source plant is a plant having or producing material (either raw or processed) that comprises stored solar energy that can be converted to fuel. In general terms, such plants comprise dedicated energy crops as well as agricultural and woody plants. Examples of biomass renewable energy source plants include: switchgrass, elephant grass, giant Chinese silver grass, energycane, giant reed (also known as wild cane), tall fescue, bermuda grass, *sorghum*, napier grass (also known as uganda grass), *triticale*, rye, winter wheat, shrub poplar, shrub willow, big bluestem, reed canary grass, and corn.

Information that the polypeptides disclosed herein can modulate low light tolerance can be useful in breeding of plants. Based on the effect of disclosed polypeptides on low light tolerance, one can search for and identify polymorphisms linked to genetic loci for such polypeptides. Polymorphisms that can be identified include simple sequence repeats (SSRs), rapid amplification of polymorphic DNA (RAPDs), amplified fragment length polymorphisms (AFLPs) and restriction fragment length polymorphisms (RFLPs).

If a polymorphism is identified, its presence and frequency in populations is analyzed to determine if it is statistically significantly correlated to an alteration in low light tolerance. Those polymorphisms that are correlated with an alteration in low light tolerance can be incorporated into a marker assisted breeding program to facilitate the development of lines that have a desired alteration in low light tolerance. Typically, a polymorphism identified in such a manner is used with polymorphisms at other loci that are also correlated with a desired alteration in low light tolerance.

Articles of Manufacture

Seeds of transgenic plants described herein can be conditioned and bagged in packaging material by means known in the art to form an article of manufacture. Packaging material such as paper and cloth are well known in the art. A package of seed can have a label e.g., a tag or label secured to the packaging material, a label printed on the packaging material, or a label inserted within the package.

Plants, plant tissues, and/or seeds from plants grown from seeds having an exogenous nucleic acid encoding a low light-

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tolerance polypeptide can be used for making products including, without limitation, human and animal foods, textiles, oils, and/or ethanol.

The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

Example 1

Transgenic Plants

The following symbols are used in the Examples: T₁: first generation transformant; T₂: second generation, progeny of self-pollinated T₁ plants; T₃: third generation, progeny of self-pollinated T₂ plants; T₄: fourth generation, progeny of self-pollinated T₃ plants. Independent transformations are referred to as events.

Ceres Clone 28780 (genomic locus At1g07090; SEQ ID NO:87) is a cDNA clone that was isolated from *Arabidopsis* and is predicted to encode a 196 amino acid polypeptide (SEQ ID NO:88) designated LSH6. Ceres Clone 28780 was cloned into a Ti plasmid vector, CRS 338, containing a phosphinothricin acetyltransferase gene, which confers transformed plants with Finale® resistance. The construct made using the CRS 338 vector contained Ceres Clone 28780 operably linked to a CaMV 35S promoter. Wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) plants were transformed with the construct containing Ceres Clone 28780. The transformation was performed essentially as described in Bechtold and Pelletier, *Methods Mol Biol.*, 82:259-66 (1998).

A transgenic *Arabidopsis* line containing Ceres Clone 28780 was designated ME05917. The presence of the vector containing Ceres Clone 28780 in the transgenic *Arabidopsis* line transformed with the vector was confirmed by Finale® resistance, polymerase chain reaction (PCR) amplification from green leaf tissue extract, and/or sequencing of PCR products.

The segregation of Finale® resistance for T₂ plants from events -01 and -08 of ME05917 was 3:1 (resistant:sensitive).

Example 2

Identification of Transgenic Plants Tolerant to Low Light Conditions

Wild-type and transgenic seeds were sterilized, plated on solid 0.5×MS medium containing 5 g/L sucrose, and stratified at 4° C. in the dark for three days. After stratification, plates containing the seeds were allowed to reach room temperature. The plates were then transferred to a Conviron walk-in growth chamber (Controlled Environments Inc., Pambina, N. Dak.) at 22° C. and 70% humidity with a 16:8 hour light:dark cycle. Lighting was supplied by 32 watt fluorescent bulbs (Sylvania, F032/841/ECO, Danvers, Mass.), providing a red:far-red ratio of 13:1. The plates were covered with three layers of shade cloth (New York wire, charcoal fiberglass screen, 857650; Home Depot, Atlanta, Ga.) such that the irradiance was about 10 μmol/m²/s. The plates were rotated daily and monitored for changes in hypocotyl elongation. After 48 hours, the plates were scored for late germinators, which were eliminated from consideration as candidate plants having reduced hypocotyl elongation under low light conditions. Each seedling was transplanted to an 8×8 cm well of a flat containing a total of 18 wells (three wells by six wells) and measuring 24 cm by 48 cm in size.

Seedlings maintained under conditions of irradiance with about 10 $\mu\text{mol}/\text{m}^2/\text{s}$ of light for seven days at 22° C. were analyzed for hypocotyl length. Transgenic seedlings having a shorter hypocotyl length than the hypocotyl length of corresponding wild-type seedlings were selected and analyzed using PCR and DNA sequencing to identify the transgenes. The transgenic *Arabidopsis* line ME05917, described in Example 1, was identified as having reduced hypocotyl elongation under the low light conditions as compared to wild-type control plants.

Example 3

Characterization of the Low Light Tolerance of Seedlings from ME05917 Events

T_2 and T_3 seedlings from events -01 and -08 of ME05917 were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl. A hypocotyl having a length similar to the hypocotyl length typically exhibited by wild-type *Arabidopsis* seedlings grown under normal light conditions (e.g., about 100 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light) was considered a short hypocotyl, whereas a hypocotyl having a length similar to that typically exhibited by wild-type *Arabidopsis* seedlings grown under low light conditions (e.g., about 10 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light) was considered a long hypocotyl. Wild-type *Arabidopsis* seeds grown for seven days at 22° C. under conditions of irradiance with about 100 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light and a 16:8 hour light:dark cycle typically form hypocotyls that are about 1-3 mm in length. Under conditions of irradiance with about 10 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light, the hypocotyls typically are about 5-7 mm in length.

Seedlings from events -01 and -08 of ME05917 displayed a short hypocotyl under low light conditions in both the T_2 and T_3 generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of $p < 0.05$ (Table 1).

TABLE 1

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	
			p-value	
T_2 seedlings from event -01 of ME05917	42	0	39.71	2.95E-10
T_2 non-transgenic segregants of event -01 of ME05917	2	8		
T_3 seedlings from event -01 of ME05917	38	2	46.93	7.37E-12
T_3 non-transgenic segregants of event -01 of ME05917	2	21		
T_2 seedlings from event -08 of ME05917	15	7	10.91	9.57E-04
T_2 non-transgenic segregants of event -08 of ME05917	0	8		
T_3 seedlings from event -08 of ME05917	37	8	43.8	3.63E-11

TABLE 1-continued

Chi-square comparison of the hypocotyl length of transgenic seedlings and non-transgenic segregants grown under low light irradiance (10 $\mu\text{mol}/\text{m}^2/\text{s}$) for seven days				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T_3 non-transgenic segregants of event -08 of ME05917	1	28		

The expression level of genomic locus At1g07090 in two week old T_3 plants from single insertion events -01-09 and -08-28 of the transgenic line ME05917 was determined using RT-PCR and quantitative RT-PCR. The plants were grown under conditions of irradiance with about 100 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light. Aerial tissue was collected from five plants from each of events -01-09 and -08-28 of ME05917 and from five corresponding non-transgenic segregant plants. The tissues were flash frozen in liquid nitrogen, and total RNA was extracted from the tissues using a plant RNeasy kit (Qiagen, Valencia, Calif.). First strand cDNA was synthesized using 1000 ng of total RNA and Superscript II (Invitrogen, Carlsbad, Calif.). PCR was performed using one μL of the first strand cDNA reaction. The PCR conditions were as follows: 94° C. for five minutes; 25 cycles of 94° C. for 30 seconds, 58° C. for one minute, and 72° C. for 40 seconds; and 72° C. for seven minutes. Expression of tubulin was measured as an internal standard. The primers used to detect expression of tubulin were: TUB-F1, 5'-GTTGAGCCGTACAATGCAAC-3' (SEQ ID NO:95) and TUB-R1, 5'-CTGTTCGTCCACT-TCCTTG-3' (SEQ ID NO:96). The primers used to detect expression of At1g07090 were: 05917-F, 5'-AGCAGGTAT-GAGTCACAGAACGGA-3' (SEQ ID NO:97) and 05917-R, 5'-ACAGATGGAGCACCGACGTACAA-3' (SEQ ID NO:98). Equal volumes of the PCR reactions were analyzed using 1% agarose gel electrophoresis. Quantitative PCR was performed using an iCycler system (BioRad, Hercules, Calif.) and standard protocols.

The expression level of At1g07090, as analyzed using RT-PCR, was elevated in T_3 plants from both events of ME05917 analyzed, -01-09 and -08-28, as compared to the expression level of At1g07090 in corresponding wild-type or non-transgenic segregant plants. Analysis of At1g07090 expression using quantitative PCR indicated that the expression level of At1g07090 was increased by 312-fold and 233-fold in ME05917 plants from events -01-09 and -08-28, respectively, compared to the expression level of At1g07090 in non-transgenic segregant plants of event -01-28 of ME05917. These results indicated that the expression level of At1g07090 in plants from event -01-09 was about 34% higher than the expression level in plants from event -08-28.

The low light tolerance, as measured by reduced hypocotyl elongation, of seedlings from ME05917 events was characterized further. T_2 seedlings from events -01 and -08 of ME05917, T_3 seedlings from single insertion events -01-09 and -08-28 of the homozygous ME05917 line, T_3 non-transgenic segregants of ME05917-01-28, and wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) seedlings were grown under conditions of irradiance with about 10 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light as described in Example 2. The hypocotyl lengths of about ten seedlings from each event were measured after seven days using digital calipers.

The average hypocotyl length of T_2 and T_3 seedlings from each event of ME05917 analyzed was significantly shorter than the average hypocotyl length of corresponding non-transgenic segregants or wild-type seedlings (Table 2).

TABLE 2

Hypocotyl length of seedlings from ME05917 events grown under conditions of irradiance with about 10 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light						
	T ₂ seedlings from event -01	T ₂ seedlings from event -08	T ₃ seedlings from event -01-09	T ₃ seedlings from event -08-28	Non-transgenic segregants of event -01-28	Wild-type seedlings
Average hypocotyl length (mm) \pm standard deviation	2.098 \pm 0.451	2.503 \pm 0.893	1.868 \pm 0.169	2.071 \pm 0.289	4.358 \pm 0.443	4.931 \pm 0.312
p-value versus non-transgenic segregants	4.54E-09	2.54E-03	2.00E-09	4.67E-10	N/A	N/A
p-value versus wild-type seedlings	2.66E-10	7.68E-04	5.43E-12	3.43E-13	N/A	N/A

T₃ seedlings from single insertion events -01-09 and -08-28 of the homozygous ME05917 line, T₃ non-transgenic segregants of ME05917-01-28, and wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) seedlings were also grown under conditions of irradiance with about 100 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light as described in Example 2. The hypocotyl lengths of about ten seedlings from each event were measured after seven days using digital calipers.

The average hypocotyl length of T₃ seedlings from each event of ME05917 analyzed was significantly shorter than the average hypocotyl length of corresponding non-transgenic segregants or wild-type seedlings (Table 3).

regants of ME05917-01-28, and wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) seedlings were also grown in the dark. The seeds were prepared as described in Example 2 and exposed to about 100 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light for two hours to promote uniform germination prior to covering the plates with aluminum foil. The seeds were grown in the dark at 22° C. and 70% humidity for five days, after which the hypocotyl lengths of about ten seedlings from each event were measured using digital calipers.

The average hypocotyl length of T₃ seedlings from each event of ME05917 analyzed was significantly shorter than the

TABLE 3

Hypocotyl length of T ₃ seedlings from ME05917 events grown under conditions of irradiance with about 100 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light				
	Event -01-09	Event -08-28	Non-transgenic segregants of event -01-28	Wild-type seedlings
Average hypocotyl length (mm) \pm standard deviation	1.535 \pm 0.232	1.754 \pm 0.183	2.187 \pm 0.356	2.077 \pm 0.224
p-value versus non-transgenic segregants	1.95E-04	4.39E-03	N/A	N/A
p-value versus wild-type seedlings	4.70E-05	2.50E-03	N/A	N/A

T₃ seedlings from single insertion events -01-09 and -08-28 of the homozygous ME05917 line, T₃ non-transgenic seg-

average hypocotyl length of corresponding non-transgenic segregants or wild-type seedlings (Table 4).

TABLE 4

Hypocotyl length of T ₃ seedlings from ME05917 events grown in the dark				
	Event -01-09	Event -08-28	Non-transgenic segregants of event -01-28	Wild-type seedlings
Average hypocotyl length (mm) \pm standard deviation	9.496 \pm 1.526	10.850 \pm 0.887	13.008 \pm 1.317	12.494 \pm 1.420
p-value versus non-transgenic segregants	1.28E-05	3.32E-04	N/A	N/A
p-value versus wild-type seedlings	1.70E-04	7.18E-03	N/A	N/A

No cotyledon phenotypes were observed in transgenic seedlings as compared to non-transgenic segregating controls (FIG. 2). Interestingly, T₃ seedlings from event -01-09 of ME05917 had a shorter average hypocotyl length than T₃ seedlings from event -08-28 of ME05917 when grown in the dark or under conditions of irradiance with about 100 µmol/m²/s of white light ($p < 0.05$). As presented above, the expression level of At1g07090 in plants from event -01-09 was higher than the expression level in plants from event -08-28. Taken together, these results suggest that reduction in hypocotyl elongation is proportional to the expression level of At1g07090 in ME05917 plants.

Example 4

Characterization of the Low Light Tolerance of Adult Plants from ME05917 Events

Seeds from transgenic ME05917 plants and corresponding control plants were sown in a checkerboard pattern in no-hole utility flats. Wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) plants and non-transgenic segregating plants were used as control plants. The flats were covered with propagation domes and maintained at 4° C. in the dark for three days. The flats were then transferred to a Conviron walk-in growth chamber (Controlled Environments Inc.) with a 16:8 hour light:dark cycle, a relative humidity of 70%, a temperature of 22° C., and an irradiance of about 150 µmol/m²/s of light having a red to far-red ratio greater than one. The propagation domes were removed after four days. After three weeks, the flats were divided into two groups of plants. One group, referred to as the normal light treatment (NLT) group, remained under the same conditions, with a 16:8 hour light:dark cycle, a relative humidity of 70%, a temperature of 22° C., and an irradiance of about 150 µmol/m²/s of light having a red to far-red ratio greater than one, for the duration of the experiment. The other group, referred to as the low light stress treatment (LLT) group, was placed under three layers of shade screen to reduce the irradiance to about 15 µmol/m²/s without altering the spectral quality. After one week, the shade screens were removed, and the low light stress treatment group was once again grown under an irradiance of about 150 µmol/m²/s.

Measurements were taken at four different stages (FIG. 3). Stage one occurred after three weeks of growth under normal light conditions (irradiance of about 150 µmol/m²/s) and before transfer of the LLT group to low light conditions (irradiance of about 15 µmol/m²/s). Stage two occurred after three weeks of growth under normal light conditions and one week of growth under low light conditions for the LLT group,

and before transfer of the LLT group back to normal light conditions. Stage three occurred one week after transfer of the LLT back to normal light conditions, when the plants were five weeks old. Stage four occurred after senescence, when the plants were eight weeks old. Photosynthetic efficiency was measured at stage two, and rosette areas were measured at stages one and two. Fresh weight was measured at stages one, two, and three. Dry weight and seed yield were determined at stage four. Six to nine replicate plant samples were measured at each stage for each treatment group, and the average values and standard deviations were calculated.

To measure photosynthetic efficiency, plants were first placed in the dark for at least 20 minutes. Rosettes were removed from the plants by cutting at the rosette-root junction. Detached rosettes were placed in the middle of the stage of a CF Imager (Technologica Ltd., Essex, UK). Chlorophyll fluorescence was measured with a pulse intensity of 4400 µmol/m²/s and a pulse length of 800 ms. The area of each rosette was also measured using the CF imager.

After measuring photosynthetic efficiency and rosette area, the rosette was removed from the CF imager and weighed along with the stem from which it was removed. The weight was recorded as the fresh weight measurement.

Seed and dry weight measurements were obtained when plants were eight weeks old. Plants were harvested individually and allowed to dry completely at 28° C. for three days. The seed was separated from the dried plant material using a sieve (300 µM mesh size) and weighed. The dried plant material was added to the seed and the combined weight was recorded as the dry weight.

Results

T₃ plants from single insertion events -01-09 and -08-28 of the homozygous ME05917 line, T₃ non-transgenic segregants of ME05917-01-28, and wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) plants were grown under conditions of irradiance with about 150 µmol/m²/s of light and analyzed to determine the number of days that elapsed between seed sowing (after stratification) and primary bolt emergence of about one cm, or days to bolt. T₃ plants from event -01-09 were not observed to differ significantly in days to bolt from corresponding non-transgenic segregant or wild-type control plants (Table 5). T₃ plants from event -08-28 also were observed to not differ significantly from non-transgenic segregants in days to bolt, whereas the average number of days to bolt for plants from event -08-28 was significantly lower than the average number of days to bolt for wild-type plants (Table 5). On average, transgenic and control plants bolted about 15 to 17 days post-germination (Table 5).

TABLE 5

Days to bolt for T ₃ plants from ME05917 events				
	Event -01-09	Event -08-28	Non-transgenic segregants of event -01-28	Wild-type <i>Arabidopsis</i> Ws plants
Average days to bolt ± standard deviation	17.267 ± 1.163	15.278 ± 1.274	16.529 ± 0.943	17.056 ± 0.791
p-value versus non-transgenic segregants	6.12E-02	5.40E-02	N/A	N/A
p-value versus wild-type plants	5.27E-01	1.49E-05	N/A	N/A

Rosette areas of T_3 plants from single insertion events -01-09 and -08-28 of the homozygous ME05917 line, T_3 non-transgenic segregants of ME05917-01-28, and wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) plants in the NLT or LLT group were analyzed at stage one (three weeks old) and stage two (four weeks old), as described above. The average rosette area of T_3 plants from events -01-09 and -08-28 of ME05917 was significantly smaller than the average rosette area of corresponding non-transgenic segregants and wild-type plants after three weeks of growth under conditions of irradiance with about 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, in the absence of any low light treatment (Table 6). As presented in Table 6, the average rosette area of plants from events -01-09 and -08-28 was about 50% smaller than the average rosette area of non-transgenic segregants, and more than 60% smaller than the average rosette area of wild-type plants under conditions of irradiance with about 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light.

At stage two, the average rosette area of plants from events -01-09 and -08-28 of ME05917 was significantly smaller than the average rosette area of control plants, regardless of whether the plants were in the LLT or the NLT group. As presented in Table 6, the average rosette area of plants from events -01-09 and -08-28 in the LLT group was about 23% and 50% smaller, respectively, than the average rosette area of non-transgenic segregants in the LLT group. The average rosette area of plants from events -01-09 and -08-28 in the NLT group was about 37% and 35% smaller, respectively, than the average rosette area of non-transgenic segregants in the NLT group (Table 6).

Although the rosette areas of plants from events -01-09 and -08-28 of ME05917 were reduced (Table 6), the photosynthetic efficiency was similar to that of non-transgenic segregating and wild-type controls. As presented in Table 7, there were no significant differences in photosynthetic efficiency between plants from events -01-09 and -08-28 of ME05917 and non-transgenic segregants or wild-type plants in the LLT or NLT group at stage two.

TABLE 6

Rosette area of T_3 plants from ME05917 events			
	Average rosette area \pm standard deviation	p-value versus non-transgenic segregants	p-value versus wild-type plants
Event -01-09 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	210.286 \pm 25.736	1.34E-07	3.01E-07
Event -01-09 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	508.171 \pm 88.517	5.66E-03	4.63E-03
Event -01-09 4 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	455.942 \pm 93.474	7.59E-04	1.42E-07
Event -08-28 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	208.410 \pm 44.842	8.91E-08	3.32E-08
Event -08-28 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	332.390 \pm 75.840	7.57E-06	3.08E-06
Event -08-28 4 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	465.543 \pm 100.938	1.55E-03	4.10E-07
Non-transgenic segregants of event -01-28 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	414.811 \pm 49.785	N/A	N/A
Non-transgenic segregants of event -01-28 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	663.623 \pm 114.433	N/A	N/A
Non-transgenic segregants of event -01-28 4 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	721.074 \pm 164.671	N/A	N/A
Wild-type <i>Arabidopsis</i> Ws plants 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	558.520 \pm 67.430	N/A	N/A
Wild-type <i>Arabidopsis</i> Ws plants 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	632.495 \pm 63.954	N/A	N/A
Wild-type <i>Arabidopsis</i> Ws plants 4 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	1003.666 \pm 122.442	N/A	N/A

TABLE 7

	Average photosynthetic efficiency \pm standard deviation	p-value versus non-transgenic segregants	p-value versus wild-type plants
Event -01-09	0.784 \pm 0.011	6.70E-01	2.12E-01
4 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light			
Event -01-09	0.769 \pm 0.009	4.07E-01	6.95E-01
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light			
Event -08-28	0.780 \pm 0.011	2.12E-01	5.12E-02
4 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light			
Event -08-28	0.768 \pm 0.010	4.19E-01	8.32E-01
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light			
Non-transgenic segregants of event -01-28	0.787 \pm 0.010	N/A	N/A
4 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light			
Non-transgenic segregants of event -01-28	0.772 \pm 0.007	N/A	N/A
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light			
Wild-type <i>Arabidopsis</i> Ws plants	0.790 \pm 0.003	N/A	N/A
4 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light			
Wild-type <i>Arabidopsis</i> Ws plants	0.767 \pm 0.007	N/A	N/A
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light			

Biomass accumulation was assessed based on measurement of the fresh weight of aerial tissues from ME05917 plants and non-transgenic segregants, as described above. The fresh weights of T_3 plants from events -01-09 and -08-28 of ME05917 were significantly less than the fresh weights of non-transgenic segregating controls in the LLT group at stages one (3 weeks old), two (four weeks old), and three (five weeks old; Table 8). In the NLT group, the fresh weights of T_3 plants from events -01-09 and -08-28 were also significantly less than the fresh weights of non-transgenic segregating controls at stages one and two (Table 8). At stage three, plants from events -01-09 and -08-28 also had fresh weights that were less than the fresh weights of non-transgenic segregating controls, but the difference was less statistically significant (Table 8).

TABLE 8

	Average fresh weight \pm standard deviation	p-value versus non-transgenic segregants
Fresh weights of three, four, and five week old T_3 plants from ME05917 events		
Event -01-09	0.155 \pm 0.031	4.27E-06
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Event -08-28	0.127 \pm 0.030	4.23E-07
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light and Non-transgenic segregants of event -01-28	0.283 \pm 0.044	N/A
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light and Event -01-09	0.583 \pm 0.090	4.92E-04
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light		
Event -08-28	0.443 \pm 0.149	1.33E-04
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light		

TABLE 8-continued

	Average fresh weight \pm standard deviation	p-value versus non-transgenic segregants
Fresh weights of three, four, and five week old T_3 plants from ME05917 events		
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light		
Event -01-09	0.841 \pm 0.144	N/A
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light, 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Event -08-28	1.786 \pm 0.534	1.25E-03
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light, 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Event -01-28	1.199 \pm 0.416	3.19E-05
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light, 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Non-transgenic segregants of event -01-28	2.686 \pm 0.429	N/A
3 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light, 1 week under 15 $\mu\text{mol/m}^2/\text{s}$ of light and 1 week under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Event -01-09	1.001 \pm 0.177	1.56E-03
4 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Event -08-28	1.136 \pm 0.213	1.91E-02
4 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Non-transgenic segregants of event -01-28	1.498 \pm 0.324	N/A
4 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Event -01-09	2.002 \pm 0.500	5.31E-02
5 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Event -08-28	2.005 \pm 0.486	5.61E-02
5 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light		
Non-transgenic segregants of event -01-28	3.050 \pm 1.347	N/A
5 weeks under 150 $\mu\text{mol/m}^2/\text{s}$ of light		

Although differences in biomass were observed between plants in the LLT and NLT group (Table 8), all of the plants appeared developmentally similar at all stages of growth through bolting, flowering, and senescence. All of the plants

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flowered prior to low light treatment (Table 5), but growth of reproductive tissue seemed to slow down during low light treatment and the stems appeared weak and spindly. Most of the biomass increases during this time appeared to be due to growth of the rosette. After one week of low light treatment, plants in the LLT group were returned to conditions of irradiance with 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light for one week. During this period, the stems of T_3 plants from events -01-09 and -08-28 of ME05917 and non-transgenic segregating control plants increased in strength, and growth of reproductive tissues seemed to accelerate. After one week of irradiance with 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, at stage three, both transgenic ME05917 plants and control plants had segments on most stems where

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siliques failed to form. No visible differences were observed between transgenic ME05917 plants and non-transgenic segregating control plants in the ability to form siliques under low light stress. All plants continued to develop normally through the termination of flowering and senescence.

After senescence, plants were collected and average dry weight, seed weight, and harvest index (total seed weight divided by total dry weight) were calculated. At harvest, T_3 plants from events -01-09 and -08-28 of ME05917 in the LLT group had average dry weights that were 31% and 42% lower, respectively, than the average dry weight of non-transgenic segregating controls in the LLT group (Table 9).

TABLE 9

Dry weight of eight week old T_3 plants from ME05917 events after senescence			
	Average dry weight \pm standard deviation	p-value versus non-transgenic segregants	p-value versus wild-type plants
Event -01-09 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, 1 week under 15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, and 4 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	0.480 \pm 0.113	2.18E-02	2.79E-03
Event -08-28 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, 1 week under 15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, and 4 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	0.407 \pm 0.125	4.54E-03	2.68E-04
Non-transgenic segregants of event -08-27 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, 1 week under 15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, and 4 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	0.695 \pm 0.218	N/A	N/A
Wild-type <i>Arabidopsis</i> Ws plants 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, 1 week under 15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, and 4 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	0.683 \pm 0.166	N/A	N/A
Event -01-09 8 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	0.535 \pm 0.188	1.15E-05	5.80E-06
Event -08-28 8 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	0.833 \pm 0.161	3.27E-04	1.12E-02
Non-transgenic segregants of event -08-27 8 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	1.463 \pm 0.267	N/A	N/A
Wild-type <i>Arabidopsis</i> Ws plants 8 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	1.082 \pm 0.295	N/A	N/A

T_3 plants from events -01-09 and -08-28 of ME05917 in the NLT group had average dry weights that were 63% and 43% lower, respectively, than the average dry weight of non-transgenic segregating controls in the NLT group (Table 9).

The average seed weight of T_3 plants from events -01-09 and -08-28 of ME05917 in the LLT group was 25% and 37% lower, respectively, than the average seed weight of non-transgenic segregating controls in the LLT group (Table 10).

TABLE 10

Seed weight of eight week old T_3 plants from ME05917 events after senescence			
	Average seed weight \pm standard deviation	p-value versus non-transgenic segregants	p-value versus wild-type plants
Event -01-09 3 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, 1 week under 15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light, and 4 weeks under 150 $\mu\text{mol}/\text{m}^2/\text{s}$ of light	0.162 \pm 0.045	3.58E-02	7.01E-04

TABLE 10-continued

Seed weight of eight week old T ₃ plants from ME05917 events after senescence			
	Average seed weight ± standard deviation	p-value versus non-transgenic segregants	p-value versus wild-type plants
Event -08-28 3 weeks under 150 μmol/m ² /s of light, 1 week under 15 μmol/m ² /s of light, and 4 weeks under 150 μmol/m ² /s of light Non-transgenic segregants of event -08-27 3 weeks under 150 μmol/m ² /s of light, 1 week under 15 μmol/m ² /s of light, and 4 weeks under 150 μmol/m ² /s of light Wild-type <i>Arabidopsis</i> Ws plants 3 weeks under 150 μmol/m ² /s of light, 1 week under 15 μmol/m ² /s of light, and 4 weeks under 150 μmol/m ² /s of light	0.136 ± 0.043	2.98E-03	2.57E-05
Event -08-28 8 weeks under 150 μmol/m ² /s of light Event -08-28 8 weeks under 150 μmol/m ² /s of light Non-transgenic segregants of event -08-27 8 weeks under 150 μmol/m ² /s of light Wild-type <i>Arabidopsis</i> Ws plants 8 weeks under 150 μmol/m ² /s of light	0.215 ± 0.052 0.245 ± 0.051 0.181 ± 0.044 0.265 ± 0.042 0.515 ± 0.077 0.397 ± 0.110	N/A N/A 3.00E-06 3.24E-05 N/A N/A	N/A N/A 1.56E-07 1.84E-04 N/A N/A

The average seed weight of T₃ plants from events -01-09 and -08-28 of ME05917 in the NLT group was 65% and 49% lower, respectively, than the average seed weight of non-transgenic segregating controls in the NLT group (Table 10).

The average harvest index of T₃ plants from events -01-09 and -08-28 of ME05917 was not observed to differ significantly from the average harvest index of non-transgenic segregating controls in the LLT or NLT group (Table 11).

TABLE 11

Harvest index of eight week old T ₃ plants from ME05917 events after senescence			
	Average harvest index ± standard deviation	p-value versus non-transgenic segregants	p-value versus wild-type plants
Event -01-09 3 weeks under 150 μmol/m ² /s of light, 1 week under 15 μmol/m ² /s of light, and 4 weeks under 150 μmol/m ² /s of light	0.337 ± 0.035	2.40E-01	8.18E-02
Event -08-28 3 weeks under 150 μmol/m ² /s of light, 1 week under 15 μmol/m ² /s of light, and 4 weeks under 150 μmol/m ² /s of light Non-transgenic segregants of event -08-27 3 weeks under 150 μmol/m ² /s of light, 1 week under 15 μmol/m ² /s of light, and 4 weeks under 150 μmol/m ² /s of light Wild-type <i>Arabidopsis</i> Ws plants 3 weeks under 150 μmol/m ² /s of light, 1 week under 15 μmol/m ² /s of light, and 4 weeks under 150 μmol/m ² /s of light	0.332 ± 0.031 0.316 ± 0.038	3.25E-01 N/A	3.22E-02 N/A
Event -01-09 8 weeks under 150 μmol/m ² /s of light Event -08-28 8 weeks under 150 μmol/m ² /s of light Non-transgenic segregants of event -08-27 8 weeks under 150 μmol/m ² /s of light Wild-type <i>Arabidopsis</i> Ws plants 8 weeks under 150 μmol/m ² /s of light	0.348 ± 0.034 0.324 ± 0.051 0.354 ± 0.020 0.367 ± 0.014	6.86E-01 1.53E-01 N/A N/A	1.56E-01 4.84E-02 N/A N/A

Overall, T₃ plants from events -01-09 and -08-28 of ME05917 were observed to have a shorter plant height at harvest than non-transgenic segregating controls or wild type plants.

Example 5

Transgenic Plants

The following DNA clones were isolated from *Arabidopsis thaliana* plants. Each of the DNA clones encodes a polypeptide that is the same as or similar to members of a family designated as the light-dependent short hypocotyls (LSH) polypeptide family (Zhao et al., *Plant J.*, 37(5):694-706 (2004)). Ceres ANNOT ID no. 832857 (genomic locus At1g16910; SEQ ID NO:111) is a DNA clone that is predicted to encode a 164 amino acid polypeptide (SEQ ID NO:112) designated LSH8. Ceres ANNOT ID no. 1290753 (genomic locus At5g28490; SEQ ID NO:101) is a DNA clone that is predicted to encode a 190 amino acid polypeptide (SEQ ID NO:102) designated LSH1. Ceres ANNOT ID no. 856813 (genomic locus At5g58500; SEQ ID NO:115) is a DNA clone that is predicted to encode a 182 amino acid polypeptide (SEQ ID NO:116) designated LSH5. Ceres ANNOT ID no. 828846 (SEQ ID NO:109) is a DNA clone that is predicted to encode a 219 amino acid polypeptide (SEQ ID NO:110) designated LSH3. Ceres CLONE ID no. 1025179 (SEQ ID NO:119) is a DNA clone that is predicted to encode a 195 amino acid polypeptide (SEQ ID NO:120) designated LSH4. Ceres ANNOT ID no. 870022 (SEQ ID NO:117) is a DNA clone that is predicted to encode a 195 amino acid polypeptide (SEQ ID NO:118) designated LSH7. Ceres ANNOT ID no. 1285138 (SEQ ID NO:99) is a DNA clone that is predicted to encode a 188 amino acid polypeptide (SEQ ID NO:100) designated LSH9. Ceres ANNOT ID no. 847799 (SEQ ID NO:113) is a DNA clone that is predicted to encode a 191 amino acid polypeptide (SEQ ID NO:114) designated LSH9.

Ceres CLONE ID no. 604111(a) (SEQ ID NO:125) and Ceres CLONE ID no. 604111(b) (SEQ ID NO:129) are DNA clones that were isolated from a *Glycine max* plant. Ceres CLONE ID no. 604111(a) (SEQ ID NO:125) is predicted to encode a 229 amino acid polypeptide (SEQ ID NO:126) designated as an orthologous LSH6 polypeptide. Ceres CLONE ID no. 604111(b) (SEQ ID NO:129) is predicted to encode a 229 amino acid polypeptide (SEQ ID NO:146) designated as an orthologous LSH6 polypeptide.

Ceres CLONE ID no. 1464359 (SEQ ID NO:123) is a DNA clone that was isolated from a *Zea mays* plant. Ceres CLONE ID no. 1464359 (SEQ ID NO:123) is predicted to encode a 183 amino acid polypeptide (SEQ ID NO:124) designated as an orthologous LSH6 polypeptide.

The following DNA clones were isolated from *Brassica napus* plants. Ceres CLONE ID no. 964932 (SEQ ID NO:127) is a DNA clone that is predicted to encode a 199 amino acid polypeptide (SEQ ID NO:128) designated as an orthologous LSH6 polypeptide. Ceres CLONE ID no. 1084747 (SEQ ID NO:121) is a DNA clone that is predicted to encode a 198 amino acid polypeptide (SEQ ID NO:122) designated as an orthologous LSH6 polypeptide.

Ceres ANNOT ID no. 1373087 (SEQ ID NO:103) is a DNA clone that was isolated from an *Oryza sativa* plant. Ceres ANNOT ID no. 1373087 (SEQ ID NO:103) is predicted to encode a 212 amino acid polypeptide (SEQ ID NO:104) designated as an orthologous LSH6 polypeptide.

The following DNA clones were isolated from *Populus balsamifera* subsp. *Trichocarpa* plants. Ceres ANNOT ID no.

1440417 (SEQ ID NO:105) is a DNA clone that is predicted to encode a 228 amino acid polypeptide (SEQ ID NO:106) designated as an orthologous LSH6 polypeptide. Ceres ANNOT ID no. 1505805 (SEQ ID NO:107) is a DNA clone that is predicted to encode a 240 amino acid polypeptide (SEQ ID NO:108) designated as an orthologous LSH6 polypeptide.

Each of Ceres ANNOT ID no. 832857, Ceres ANNOT ID no. 1290753, Ceres ANNOT ID no. 856813, Ceres ANNOT ID no. 828846, Ceres ANNOT ID no. 870022, Ceres ANNOT ID no. 1285138, Ceres ANNOT ID no. 847799, Ceres CLONE ID no. 604111(a), Ceres CLONE ID no. 1464359, Ceres CLONE ID no. 964932, Ceres CLONE ID no. 1084747, Ceres ANNOT ID no. 1373087, Ceres ANNOT ID no. 1440417, and Ceres ANNOT ID no. 1505805 was cloned into a Ti plasmid vector, CRS 338, containing a phosphinothricin acetyltransferase gene, which confers transformed plants with Finale® resistance. The constructs made using the CRS 338 vector contained Ceres ANNOT ID no. 832857, Ceres ANNOT ID no. 1290753, Ceres ANNOT ID no. 856813, Ceres ANNOT ID no. 828846, Ceres ANNOT ID no. 870022, Ceres ANNOT ID no. 1285138, Ceres ANNOT ID no. 847799, Ceres CLONE ID no. 604111(a), Ceres CLONE ID no. 1464359, Ceres CLONE ID no. 964932, Ceres CLONE ID no. 1084747, Ceres ANNOT ID no. 1373087, Ceres ANNOT ID no. 1440417, or Ceres ANNOT ID no. 1505805, each operably linked to a CaMV 35S promoter. Constructs also were made using CRS 338 that contained Ceres CLONE ID no. 1025179, Ceres CLONE ID no. 604111(a), or Ceres CLONE ID no. 604111(b), each operably linked to a p326 promoter. Wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) plants were transformed separately with each construct containing Ceres ANNOT ID no. 832857, Ceres ANNOT ID no. 1290753, Ceres ANNOT ID no. 856813, Ceres ANNOT ID no. 828846, Ceres CLONE ID no. 1025179, Ceres ANNOT ID no. 870022, Ceres ANNOT ID no. 1285138, Ceres ANNOT ID no. 847799, Ceres CLONE ID no. 604111(a), Ceres CLONE ID no. 604111(b), Ceres CLONE ID no. 1464359, Ceres CLONE ID no. 964932, Ceres CLONE ID no. 1084747, Ceres ANNOT ID no. 1373087, Ceres ANNOT ID no. 1440417, or Ceres ANNOT ID no. 1505805. The transformations were performed essentially as described in Bechtold and Pelletier, *Methods Mol Biol.*, 82:259-66 (1998). The following information about each transgenic *Arabidopsis* line is presented in Table 12: DNA clone, sequence identifier of the nucleotide sequence of the DNA clone, sequence identifier of the amino acid sequence of the polypeptide encoded by the DNA clone, the promoter operably linked to the DNA clone, and the designation of the transgenic line.

TABLE 12

Transgenic <i>Arabidopsis</i> lines				
DNA clone	DNA SEQ ID NO:	Amino acid SEQ ID NO:	Promoter	Transgenic line designation
Ceres ANNOT ID no. 832857	111	112	CaMV 35S	ME23423
Ceres ANNOT ID no. 856813	115	116	CaMV 35S	ME23517
Ceres ANNOT ID no. 1290753	101	102	CaMV 35S	ME23453 ME16623
Ceres ANNOT ID no. 828846	109	110	CaMV 35S	ME25288

TABLE 12-continued

Transgenic <i>Arabidopsis</i> lines			
DNA clone	DNA SEQ ID NO:	Amino acid SEQ ID NO:	Transgenic line designation
		Promoter	
Ceres CLONE ID no. 1025179	119	120	p326 ME24513 ME24480 ME24762
Ceres ANNOT ID no. 870022	117	118	CaMV 35S ME16579
Ceres ANNOT ID no. 1285138	99	100	CaMV 35S ME16572
Ceres ANNOT ID no. 847799	113	114	CaMV 35S ME23459
Ceres CLONE ID no. 604111(a)	125	126	CaMV 35S ME25680 ME24978
Ceres CLONE ID no. 604111(a)	125	126	p326 ME24758
Ceres CLONE ID no. 604111(b)	129	146	p326 ME24507
Ceres CLONE ID no. 1464359	123	124	CaMV 35S ME25661
Ceres CLONE ID no. 964932	127	128	CaMV 35S ME25647
Ceres CLONE ID no. 1084747	121	122	CaMV 35S ME25665
Ceres ANNOT ID no. 1373087	103	104	CaMV 35S ME25698
Ceres ANNOT ID no. 1440417	105	106	CaMV 35S ME25953
Ceres ANNOT ID no. 1505805	107	108	CaMV 35S ME25957

The presence of the vector containing Ceres ANNOT ID no. 832857, Ceres ANNOT ID no. 1290753, Ceres ANNOT ID no. 856813, Ceres CLONE ID no. 1025179, Ceres ANNOT ID no. 870022, Ceres ANNOT ID no. 1285138, Ceres ANNOT ID no. 847799, Ceres CLONE ID no. 1464359, Ceres CLONE ID no. 964932, or Ceres CLONE ID no. 1084747 in each transgenic *Arabidopsis* line transformed with the vector was confirmed by Finale® resistance, polymerase chain reaction (PCR) amplification from green leaf tissue extract, and/or sequencing of PCR products. The presence of the vector containing Ceres ANNOT ID no. 828846, Ceres ANNOT ID no. 1373087, Ceres ANNOT ID no. 1440417, or Ceres ANNOT ID no. 1505805 in each transgenic *Arabidopsis* line transformed with the vector was confirmed by Finale® resistance, polymerase chain reaction (PCR) amplification from green leaf tissue extract, and/or partial sequencing of PCR products. The presence of the vector containing Ceres CLONE ID no. 604111(a) in transgenic *Arabidopsis* lines ME25680 and ME24978 was confirmed by Finale® resistance, polymerase chain reaction (PCR) amplification from green leaf tissue extract, and/or sequencing of PCR products. The presence of the vector containing Ceres CLONE ID no. 604111(a) in transgenic *Arabidopsis* line ME24758 was confirmed by Finale® resistance, polymerase chain reaction (PCR) amplification from green leaf tissue extract, and/or partial sequencing of PCR products. The presence of the vector containing Ceres CLONE ID no. 604111(b) in transgenic *Arabidopsis* line ME24507 was confirmed by Finale® resistance, polymerase chain reaction (PCR) amplification from green leaf tissue extract, and/or sequencing of PCR products.

The segregation of Finale® resistance for T₂ plants from events -02, -03, and -04 of ME23423 was 3:1 (resistant: sensitive), and the segregation for T₂ plants from event -01 of ME23423 was 15:1. The segregation of Finale® resistance for T₂ plants from events -01, -02, and -03 of ME23517 was

15:1, 3:1, and 2:1, respectively. The segregation of Finale® resistance for T₂ plants from events -02, -04, and -05 of ME23453 was 3:1.

Wild-type seeds and seeds from transgenic lines 5 ME23423, ME23517, ME25288, ME16579, ME16572, ME23459, ME25661, ME25647, ME25665, ME25698, ME25953, ME25957, ME16623, ME23453, ME24513, ME24480, ME24762, ME25680, ME24978, ME24758, and ME24507 were plated as described in Example 2. Seedlings 10 maintained under conditions of irradiance with about 10 μmol/m²/s of light for seven days at 22° C. were analyzed for hypocotyl length. The transgenic *Arabidopsis* lines ME23423, ME23517, ME25288, ME16579, ME16572, ME23459, ME25661, ME25647, ME25665, ME25698, ME25953, ME25957, ME16623, ME23453, ME24513, ME24480, ME24762, ME25680, ME24978, ME24758, and ME24507 were identified as having reduced hypocotyl elongation under the low light conditions as compared to wild-type control plants.

Example 6

Characterization of the Low Light Tolerance of Seedlings from ME23423 Events

T₂ and T₃ seedlings from events -01, -02, -03, -04, and -08, and T₂ seedlings from events -07 and -09, of ME23423 containing Ceres ANNOT ID no. 832857 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01, -02, -03, -04, and -08 of ME23423 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and seedlings from events -07 and -09 displayed a short hypocotyl under low light conditions in the T₂ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 13).

TABLE 13

Chi-square comparison of the hypocotyl length of ME23423 transgenic seedlings and non-transgenic segregants grown under low light irradiance (10 μmol/m ² /s) for seven days					
	Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
50	T ₂ seedlings from event -01	29	6	12.93	3.24E-04
	T ₂ non-transgenic segregants of event -01	0	4		
55	T ₃ seedlings from event -01-99	42	2	34.72	3.80E-09
	T ₃ non-transgenic segregants of event -01-99	1	8		
60	T ₂ seedlings from event -02	19	10	9.17	2.46E-03
	T ₂ non-transgenic segregants of event -02	1	9		
65	T ₃ seedlings from event -02-99	59	4	38.63	5.13E-10
	T ₃ non-transgenic segregants of event -02-99	1	8		
	T ₂ seedlings from event -03	20	13	3.94	4.70E-02
	T ₂ non-transgenic segregants of event -03	1	5		
	T ₃ seedlings from event -03-99	38	3	23.44	1.29E-06
	T ₃ non-transgenic segregants of event -03-99	5	11		

TABLE 13-continued

Chi-square comparison of the hypocotyl length of ME23423 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -04	26	2	25.28	4.96E-07
T ₂ non-transgenic segregants of event -04	0	7		
T ₃ seedlings from event -04-99	55	5	38.36	5.89E-10
T ₃ non-transgenic segregants of event -04-99	0	8		
T ₂ seedlings from event -07	56	4	10.96	9.29E-04
T ₂ non-transgenic segregants of event -07	12	7		
T ₂ seedlings from event -08	65	7	26.8	2.26E-07
T ₂ non-transgenic segregants of event -08	1	6		
T ₃ seedlings from event -08-99	43	9	4.32	3.77E-02
T ₃ non-transgenic segregants of event -08-99	1	2		
T ₂ seedlings from event -09	52	6	38.26	6.18E-10
T ₂ non-transgenic segregants of event -09	3	16		

The physical appearances of T₁ ME23423 plants were similar to those of corresponding control plants. There were no observable or statistically significant differences between T₂ ME23423 and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture.

Example 7

Characterization of the Low Light Tolerance of Seedlings from ME23517 Events

T₂ and T₃ seedlings from events -01, -02, and -03 of ME23517 containing Ceres ANNOT ID no. 856813 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01, -02, and -03 of ME23517 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 14).

TABLE 14

Chi-square comparison of the hypocotyl length of ME23517 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	77	0	79	6.21E-19
T ₂ non-transgenic segregants of event -01	0	2		
T ₃ seedlings from event -01-99	13	1	12.57	3.92E-04
T ₃ non-transgenic segregants of event -01-99	3	9		

TABLE 14-continued

Chi-square comparison of the hypocotyl length of ME23517 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -02	57	2	64.23	1.11E-15
T ₂ non-transgenic segregants of event -02	1	19		
T ₃ seedlings from event -02-99	14	1	12.8	3.74E-04
T ₃ non-transgenic segregants of event -02-99	2	7		
T ₂ seedlings from event -03	42	2	53.36	2.78E-13
T ₂ non-transgenic segregants of event -03	4	28		
T ₃ seedlings from event -03-99	16	3	18.84	1.42E-05
T ₃ non-transgenic segregants of event -03-99	2	15		

The physical appearances of T₁ ME23517 plants were similar to those of corresponding control plants. There were no observable or statistically significant differences between T₂ ME23517 and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture.

Example 8

Characterization of the Low Light Tolerance of Seedlings from ME23453 and ME16623 Events

T₂ and T₃ seedlings from events -02, -04, and -05, and T₃ seedlings from event -03, of ME23453 containing Ceres ANNOT ID no. 1290753 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -02, -04, and -05 of ME23453 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and seedlings from event -03 displayed a short hypocotyl under low light conditions in the T₃ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 15).

TABLE 15

Chi-square comparison of the hypocotyl length of ME23453 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -02	52	0	62.49	2.68E-15
T ₂ non-transgenic segregants of event -02	4	23		
T ₃ seedlings from event -02-99	33	0	27.79	1.35E-07
T ₃ non-transgenic segregants of event -02-99	5	10		
T ₃ seedlings from event -03-99	27	1	19.28	1.13E-05
T ₃ non-transgenic segregants of event -03-99	1	4		
T ₂ seedlings from event -04	63	0	68.42	1.32E-16
T ₂ non-transgenic segregants of event -04	2	15		

TABLE 15-continued

Chi-square comparison of the hypocotyl length of ME23453 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol}/\text{m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₃ seedlings from event -04-99	30	0	43	5.47E-11
T ₃ non-transgenic segregants of event -04-99	0	13		
T ₂ seedlings from event -05	50	2	54.45	1.59E-13
T ₂ non-transgenic segregants of event -05	3	21		
T ₃ seedlings from event -05-99	13	0	9.45	2.11E-03
T ₃ non-transgenic segregants of event -05-99	5	6		

T₁ ME23453 plants exhibited a late flowering phenotype as compared to corresponding control plants. There were no observable or statistically significant differences between T₂ ME23453 and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture.

T₂ and T₃ seedlings from events -03 and -04, and T₂ seedlings from event -02, of ME16623 containing Ceres ANNOT ID no. 1290753 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -03 and -04 of ME16623 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and seedlings from event -02 displayed a short hypocotyl under low light conditions in the T₂ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 16).

TABLE 16

Chi-square comparison of the hypocotyl length of ME16623 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol}/\text{m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -02	56	3	53.68	2.63E-13
T ₂ non-transgenic segregants of event -02	2	17		
T ₂ seedlings from event -03	48	4	24.62	7.00E-07
T ₂ non-transgenic segregants of event -03	4	9		
T ₃ seedlings from event -03-99	39	6	9.53	2.02E-03
T ₃ non-transgenic segregants of event -03-99	9	9		
T ₂ seedlings from event -04	56	3	61.32	4.86E-15
T ₂ non-transgenic segregants of event -04	0	17		
T ₃ seedlings from event -04-99	13	3	7.72	5.47E-03
T ₃ non-transgenic segregants of event -04-99	0	3		

Example 9

Characterization of the Low Light Tolerance of Seedlings from ME25288 Events

T₂ and T₃ seedlings from event -02 of ME25288 containing Ceres ANNOT ID no. 828846 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from event -02 of ME25288 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 17).

TABLE 17

Chi-square comparison of the hypocotyl length of ME25288 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol}/\text{m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -02	35	5	10.11	1.48E-03
T ₂ non-transgenic segregants of event -02	3	5		
T ₃ seedlings from event -02-99	39	6	24.73	6.58E-07
T ₃ non-transgenic segregants of event -02-99	2	11		

Example 10

Characterization of the Low Light Tolerance of Seedlings from ME24513, ME24480, and ME24762 Events

T₂ and T₃ seedlings from events -01, -02, -03, and -08 of ME24513 containing Ceres CLONE ID no. 1025179 operably linked to a p326 promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01, -02, -03, and -08 of ME24513 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 18).

TABLE 18

Chi-square comparison of the hypocotyl length of ME24513 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol}/\text{m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	53	2	59.52	1.21E-14
T ₂ non-transgenic segregants of event -01	0	15		
T ₃ seedlings from event -01-99	17	0	19	1.31E-05
T ₃ non-transgenic segregants of event -01-99	0	2		

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TABLE 18-continued

Chi-square comparison of the hypocotyl length of ME24513 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -02	43	17	14.13	1.70E-04
T ₂ non-transgenic segregants of event -02	4	14		
T ₃ seedlings from event -02-99	50	0	34.64	3.97E-09
T ₃ non-transgenic segregants of event -02-99	1	2		
T ₂ seedlings from event -03	55	2	33.69	6.46E-09
T ₂ non-transgenic segregants of event -03	8	13		
T ₃ seedlings from event -03-99	15	0	18	2.21E-05
T ₃ non-transgenic segregants of event -03-99	0	3		
T ₂ seedlings from event -08	50	14	21.07	4.44E-06
T ₂ non-transgenic segregants of event -08	2	12		
T ₃ seedlings from event -08-99	34	4	8.1	4.43E-03
T ₃ non-transgenic segregants of event -08-99	5	5		

T₂ and T₃ seedlings from events -02, -04, and -05, and T₂ seedlings from events -01 and -07, of ME24480 containing Ceres CLONE ID no. 1025179 operably linked to a p326 promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -02, -04, and -05 of ME24480 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and seedlings from events -01 and -07 displayed a short hypocotyl under low light conditions in the T₂ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of $p \leq 0.05$ (Table 19).

TABLE 19

Chi-square comparison of the hypocotyl length of ME24480 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	39	2	23.46	1.28E-06
T ₂ non-transgenic segregants of event -01	3	7		
T ₂ seedlings from event -02	36	1	5.26	2.19E-02
T ₂ non-transgenic segregants of event -02	6	2		
T ₃ seedlings from event -02-99	16	0	19	1.31E-05
T ₃ non-transgenic segregants of event -02-99	0	3		
T ₂ seedlings from event -04	24	3	11.19	8.21E-04
T ₂ non-transgenic segregants of event -04	5	8		
T ₃ seedlings from event -04-99	23	0	24.22	8.61E-07
T ₃ non-transgenic segregants of event -04-99	8	17		
T ₂ seedlings from event -05	38	0	23.62	1.17E-06
T ₂ non-transgenic segregants of event -05	4	5		

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TABLE 19-continued

Chi-square comparison of the hypocotyl length of ME24480 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₃ seedlings from event -05-99	26	0	18.72	1.51E-05
T ₃ non-transgenic segregants of event -05-99	4	6		
T ₂ seedlings from event -07	41	0	15.58	7.89E-05
T ₂ non-transgenic segregants of event -07	16	8		

T₂ and T₃ seedlings from events -01, -02, -03, -04, -05, and -06 of ME24762 containing Ceres CLONE ID no. 1025179 operably linked to a p326 promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01, -02, -03, -04, -05, and -06 of ME24762 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of $p \leq 0.05$ (Table 20).

TABLE 20

Chi-square comparison of the hypocotyl length of ME24762 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	53	2	46.93	7.34E-12
T ₂ non-transgenic segregants of event -01	1	10		
T ₃ seedlings from event -01-99	41	0	38.81	4.67E-10
T ₃ non-transgenic segregants of event -01-99	8	18		
T ₂ seedlings from event -02	44	0	57.25	3.83E-14
T ₂ non-transgenic segregants of event -02	1	17		
T ₃ seedlings from event -02-99	31	1	40.57	1.90E-10
T ₃ non-transgenic segregants of event -02-99	1	16		
T ₂ seedlings from event -03	39	1	43	5.48E-11
T ₂ non-transgenic segregants of event -03	0	9		
T ₃ seedlings from event -03-99	45	0	45.37	1.63E-11
T ₃ non-transgenic segregants of event -03-99	1	7		
T ₂ seedlings from event -04	46	5	8.63	3.30E-03
T ₂ non-transgenic segregants of event -04	10	7		
T ₃ seedlings from event -04-99	45	7	14.28	1.58E-04
T ₃ non-transgenic segregants of event -04-99	0	3		
T ₂ seedlings from event -05	42	0	54.41	1.63E-13
T ₂ non-transgenic segregants of event -05	2	19		
T ₃ seedlings from event -05-99	51	2	47.24	6.27E-12
T ₃ non-transgenic segregants of event -05-99	1	11		

TABLE 20-continued

Chi-square comparison of the hypocotyl length of ME24762 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -06	23	0	9.55	2.00E-03
T ₂ non-transgenic segregants of event -06	11	6		
T ₃ seedlings from event -06-99	37	1	13.38	2.54E-04
T ₃ non-transgenic segregants of event -06-99	5	4		

Example 11

Characterization of the Low Light Tolerance of Seedlings from ME16579 Events

T₂ and T₃ seedlings from event -07, T₃ seedlings from event -02, and T₃ and T₄ seedlings from event -05 of ME16579 containing Ceres ANNOT ID no. 870022 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from event -07 of ME16579 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, seedlings from event -02 displayed a short hypocotyl under low light conditions in the T₃ generation, and seedlings from event -05 displayed a short hypocotyl under low light conditions in the T₃ and T₄ generations. The transgene was linked to the short hypocotyl phenotype with a confidence level of $p \leq 0.05$ (Table 21).

TABLE 21

Chi-square comparison of the hypocotyl length of ME16579 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₃ seedlings from event -02-99	6	11	3.85	4.97E-02
T ₃ non-transgenic segregants of event -02-99	39	24		
T ₃ seedlings from event -05-99	42	0	57	4.36E-14
T ₃ non-transgenic segregants of event -05-99	0	15		
T ₄ seedlings from event -05-99-99	60	1	58.52	2.01E-14
T ₄ non-transgenic segregants of event -05-99-99	0	7		
T ₂ seedlings from event -07	26	1	24.58	7.14E-07
T ₂ non-transgenic segregants of event -07	1	7		
T ₃ seedlings from event -07-99	59	0	73.8	8.65E-18
T ₃ non-transgenic segregants of event -07-99	1	19		

Example 12

Characterization of the Low Light Tolerance of Seedlings from ME16572 Events

5 T₂ and T₃ seedlings from events -01, -04, and -05, and T₂ seedlings from events -02 and -03, of ME16572 containing Ceres ANNOT ID no. 1285138 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

10 Seedlings from events -01, -04, and -05 of ME16572 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and seedlings from events -02 and -03 displayed a short hypocotyl under low light conditions in the T₂ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of $p \leq 0.05$ (Table 22).

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TABLE 22

Chi-square comparison of the hypocotyl length of ME16572 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	46	9	6.23	1.25E-02
T ₂ non-transgenic segregants of event -01	3	4		
T ₃ seedlings from event -01-99	27	3	6.98	8.27E-03
T ₃ non-transgenic segregants of event -01-99	0	1		
T ₂ seedlings from event -02	21	0	45.8	1.31E-11
T ₂ non-transgenic segregants of event -02	7	43		
T ₂ seedlings from event -03	57	5	37.53	9.02E-10
T ₂ non-transgenic segregants of event -03	2	11		
T ₂ seedlings from event -04	37	3	16.49	4.90E-05
T ₂ non-transgenic segregants of event -04	8	10		
T ₃ seedlings from event -04-99	20	2	6.97	8.29E-03
T ₃ non-transgenic segregants of event -04-99	0	1		
T ₂ seedlings from event -05	64	0	24.58	7.11E-07
T ₂ non-transgenic segregants of event -05	7	4		
T ₃ seedlings from event -05-99	39	3	6.49	1.08E-02
T ₃ non-transgenic segregants of event -05-99	7	4		

Example 13

Characterization of the Low Light Tolerance of Seedlings from ME23459 Events

55 T₂ and T₃ seedlings from events -02, -05, and -08, and T₂ seedlings from event -04, of ME23459 containing Ceres ANNOT ID no. 847799 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

60 Seedlings from events -02, -05, and -08 of ME23459 displayed a short hypocotyl under low light conditions in both

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the T₂ and T₃ generations, and seedlings from event -04 displayed a short hypocotyl under low light conditions in the T₂ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 23).

TABLE 23

Chi-square comparison of the hypocotyl length of ME23459 transgenic seedlings and non-transgenic segregants grown under low light irradiance (10 μmol/m ² /s) for seven days				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -02	52	3	32.79	1.03E-08
T ₂ non-transgenic segregants of event -02	7	14		
T ₃ seedlings from event -02-99	53	1	64.66	8.89E-16
T ₃ non-transgenic segregants of event -02-99	0	16		
T ₂ seedlings from event -04	62	3	18.73	1.50E-05
T ₂ non-transgenic segregants of event -04	5	5		
T ₂ seedlings from event -05	64	0	52.44	4.44E-13
T ₂ non-transgenic segregants of event -05	4	10		
T ₃ seedlings from event -05-99	44	1	36.81	1.30E-09
T ₃ non-transgenic segregants of event -05-99	7	16		
T ₂ seedlings from event -08	63	0	74.12	7.36E-18
T ₂ non-transgenic segregants of event -08	1	16		
T ₃ seedlings from event -08-99	54	1	54.61	1.47E-13
T ₃ non-transgenic segregants of event -08-99	2	14		

Example 14

Characterization of the Low Light Tolerance of Seedlings from ME25680, ME24978, ME24758, and ME24507 Events

T₂ and T₃ seedlings from events -01, -04, -06, -07, -08, -09, and -10 of ME25680 containing Ceres CLONE ID no. 604111(a) operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01, -04, -06, -07, -08, -09, and -10 of ME25680 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 24).

TABLE 24

Chi-square comparison of the hypocotyl length of ME25680 transgenic seedlings and non-transgenic segregants grown under low light irradiance (10 μmol/m ² /s) for seven days				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	54	1	34.65	3.95E-09
T ₂ non-transgenic segregants of event -01	9	13		
T ₃ seedlings from event -01-99	58	7	20.43	6.20E-06

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TABLE 24-continued

Chi-square comparison of the hypocotyl length of ME25680 transgenic seedlings and non-transgenic segregants grown under low light irradiance (10 μmol/m ² /s) for seven days					
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value	
T ₃ non-transgenic segregants of event -01-99	5	9			
T ₂ seedlings from event -04	43	14	22.24	2.40E-06	
T ₂ non-transgenic segregants of event -04	1	13			
T ₃ seedlings from event -04-99	46	5	7.61	5.81E-03	
T ₃ non-transgenic segregants of event -04-99	9	6			
T ₂ seedlings from event -06	60	2	29.96	4.41E-08	
T ₂ non-transgenic segregants of event -06	8	10			
T ₃ seedlings from event -06-99	62	7	34.14	5.12E-09	
T ₃ non-transgenic segregants of event -06-99	0	7			
T ₂ seedlings from event -07	49	7	30.22	3.86E-08	
T ₂ non-transgenic segregants of event -07	4	15			
T ₃ seedlings from event -07-99	57	4	17.17	3.42E-05	
T ₃ non-transgenic segregants of event -07-99	7	7			
T ₂ seedlings from event -08	57	5	20.05	7.54E-06	
T ₂ non-transgenic segregants of event -08	7	9			
T ₃ seedlings from event -08-99	13	1	14.7	1.26E-04	
T ₃ non-transgenic segregants of event -08-99	0	5			
T ₂ seedlings from event -09	50	8	41.69	1.07E-10	
T ₂ non-transgenic segregants of event -09	2	20			
T ₃ seedlings from event -09-99	57	0	46.98	7.16E-12	
T ₃ non-transgenic segregants of event -09-99	3	8			
T ₂ seedlings from event -10	49	20	11.46	7.11E-04	
T ₂ non-transgenic segregants of event -10	2	9			
T ₃ seedlings from event -10-99	49	12	14.71	1.25E-04	
T ₃ non-transgenic segregants of event -10-99	4	10			

T₂ and T₃ seedlings from event -01, and T₃ seedlings from events -02 and -03, of ME24978 containing Ceres CLONE ID no. 604111(a) operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from event -01 of ME24978 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and seedlings from events -02 and -03 displayed a short hypocotyl under low light conditions in the T₃ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 25).

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TABLE 25

Chi-square comparison of the hypocotyl length of ME24978 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	47	1	44.01	3.27E-11
T ₂ non-transgenic segregants of event -01	3	13		
T ₃ seedlings from event -01-99	51	5	30.81	2.85E-08
T ₃ non-transgenic segregants of event -01-99	3	11		
T ₃ seedlings from event -02-99	50	11	15.34	8.97E-05
T ₃ non-transgenic segregants of event -02-99	1	6		
T ₃ seedlings from event -03-99	54	2	15.53	8.12E-05
T ₃ non-transgenic segregants of event -03-99	7	5		

T₂ and T₃ seedlings from event -03, and T₂ seedlings from event -01, of ME24758 containing Ceres CLONE ID no. 604111(a) operably linked to a p326 promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from event -03 of ME24758 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and seedlings from event -01 displayed a short hypocotyl under low light conditions in the T₂ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 26).

TABLE 26

Chi-square comparison of the hypocotyl length of ME24758 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	55	4	15.04	1.06E-04
T ₂ non-transgenic segregants of event -01	8	7		
T ₂ seedlings from event -03	54	2	39.72	2.93E-10
T ₂ non-transgenic segregants of event -03	5	13		
T ₃ seedlings from event -03-99	13	1	20.26	6.76E-06
T ₃ non-transgenic segregants of event -03-99	0	10		

T₂ and T₃ seedlings from events -01, -03, -05, and -09, T₂ seedlings from event -02, and T₃ seedlings from event -10 of ME24507 containing Ceres CLONE ID no. 604111(b) operably linked to a p326 promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01, -03, -05, and -09 of ME24507 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, seedlings from event -02 displayed a short hypocotyl under low light conditions in the T₂ generation, and seedlings from event -10 displayed a short hypo-

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cotyl under low light conditions in the T₃ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 27).

TABLE 27

Chi-square comparison of the hypocotyl length of ME24507 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	21	4	8.73	3.13E-03
T ₂ non-transgenic segregants of event -01	1	4		
T ₃ seedlings from event -01-99	28	0	22.65	1.95E-06
T ₃ non-transgenic segregants of event -01-99	6	10		
T ₂ seedlings from event -02	42	8	4.67	3.08E-02
T ₂ non-transgenic segregants of event -02	12	8		
T ₂ seedlings from event -03	46	13	38.52	5.41E-10
T ₂ non-transgenic segregants of event -03	0	21		
T ₃ seedlings from event -03-99	35	2	13.19	2.81E-04
T ₃ non-transgenic segregants of event -03-99	6	6		
T ₂ seedlings from event -05	42	11	30.39	3.54E-08
T ₂ non-transgenic segregants of event -05	4	23		
T ₃ seedlings from event -05-99	42	4	28.69	8.51E-08
T ₃ non-transgenic segregants of event -05-99	8	18		
T ₂ seedlings from event -09	70	6	24.25	8.44E-07
T ₂ non-transgenic segregants of event -09	0	3		
T ₃ seedlings from event -09-99	47	2	39.57	3.71E-10
T ₃ non-transgenic segregants of event -09-99	0	6		
T ₃ seedlings from event -10-99	54	6	8.28	4.02E-03
T ₃ non-transgenic segregants of event -10-99	1	2		

Example 15

Characterization of the Low Light Tolerance of Seedlings from ME25661 Events

T₂ and T₃ seedlings from events -01, -02, -03, -04, -05, and -09 of ME25661 containing Ceres CLONE ID no. 1464359 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01, -02, -03, -04, -05, and -09 of ME25661 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 28).

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TABLE 28

Chi-square comparison of the hypocotyl length of ME25661 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	61	0	52.73	3.82E-13
T ₂ non-transgenic segregants of event -01	5	13		
T ₃ seedlings from event -01-99	37	0	29.82	4.75E-08
T ₃ non-transgenic segregants of event -01-99	2	5		
T ₂ seedlings from event -02	61	1	58.23	2.34E-14
T ₂ non-transgenic segregants of event -02	3	15		
T ₃ seedlings from event -02-99	55	0	40.66	1.81E-10
T ₃ non-transgenic segregants of event -02-99	5	9		
T ₂ seedlings from event -03	61	2	37.24	1.04E-09
T ₂ non-transgenic segregants of event -03	6	11		
T ₃ seedlings from event -03-99	48	9	17.56	2.78E-05
T ₃ non-transgenic segregants of event -03-99	6	12		
T ₂ seedlings from event -04	57	0	79	6.21E-19
T ₂ non-transgenic segregants of event -04	0	22		
T ₃ seedlings from event -04-99	53	3	35.12	3.10E-09
T ₃ non-transgenic segregants of event -04-99	7	15		
T ₂ seedlings from event -05	53	3	58.9	1.66E-14
T ₂ non-transgenic segregants of event -05	1	20		
T ₃ seedlings from event -05-99	61	1	66.22	4.04E-16
T ₃ non-transgenic segregants of event -05-99	1	15		
T ₂ seedlings from event -09	53	1	71.35	2.99E-17
T ₂ non-transgenic segregants of event -09	0	22		
T ₃ seedlings from event -09-99	65	0	72.25	1.90E-17
T ₃ non-transgenic segregants of event -09-99	1	13		

Example 16

Characterization of the Low Light Tolerance of Seedlings from ME25647 Events

T₂ and T₃ seedlings from events -01, -03, -04, -05, -06, -08, -09, and -10 of ME25647 containing Ceres CLONE ID no. 964932 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01, -03, -04, -05, -06, -08, -09, and -10 of ME25647 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 29).

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TABLE 29

Chi-square comparison of the hypocotyl length of ME25647 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol/m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	39	1	68.19	1.49E-16
T ₂ non-transgenic segregants of event -01	1	35		
T ₃ seedlings from event -01-99	19	0	22.19	2.47E-06
T ₃ non-transgenic segregants of event -01-99	10	21		
T ₂ seedlings from event -03	45	17	16.89	3.97E-05
T ₂ non-transgenic segregants of event -03	3	14		
T ₃ seedlings from event -03-99	39	12	29.83	4.71E-08
T ₃ non-transgenic segregants of event -03-99	1	19		
T ₂ seedlings from event -04	62	0	60.45	7.55E-15
T ₂ non-transgenic segregants of event -04	3	13		
T ₃ seedlings from event -04-99	38	0	40.71	1.77E-10
T ₃ non-transgenic segregants of event -04-99	1	8		
T ₂ seedlings from event -05	55	1	68.85	1.06E-16
T ₂ non-transgenic segregants of event -05	0	18		
T ₃ seedlings from event -05-99	48	0	42.35	7.62E-11
T ₃ non-transgenic segregants of event -05-99	3	9		
T ₂ seedlings from event -06	55	2	46.05	1.15E-11
T ₂ non-transgenic segregants of event -06	2	11		
T ₃ seedlings from event -06-99	51	7	19.89	8.22E-06
T ₃ non-transgenic segregants of event -06-99	5	10		
T ₂ seedlings from event -08	54	0	73	1.30E-17
T ₂ non-transgenic segregants of event -08	0	19		
T ₃ seedlings from event -08-99	68	1	37.19	1.07E-09
T ₃ non-transgenic segregants of event -08-99	3	5		
T ₂ seedlings from event -09	51	6	53	3.34E-13
T ₂ non-transgenic segregants of event -09	0	20		
T ₃ seedlings from event -09-99	44	5	38.67	5.03E-10
T ₃ non-transgenic segregants of event -09-99	0	12		
T ₂ seedlings from event -10	62	8	21.85	2.95E-06
T ₂ non-transgenic segregants of event -10	0	4		
T ₃ seedlings from event -10-99	61	6	36.28	1.71E-09
T ₃ non-transgenic segregants of event -10-99	0	7		

Example 17

Characterization of the Low Light Tolerance of Seedlings from ME25665 Events

T₂ and T₃ seedlings from events -03, -06, and -08, and T₂ seedlings from event -04, of ME25665 containing Ceres CLONE ID no. 1084747 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -03, -06, and -08 of ME25665 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and seedlings from event -04 displayed a short hypocotyl under low light conditions in the T₂ generation. The transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 30).

TABLE 30

Plants	Short	Long	Chi-	p-value
	Hypocotyl	Hypocotyl	Square	
T ₂ seedlings from event -03	58	18	11.1	8.63E-04
T ₂ non-transgenic	0	4		
segregants of event -03				
T ₃ seedlings from event -03-99	57	4	11.59	6.64E-04
T ₃ non-transgenic	0	1		
segregants of event -03-99				
T ₂ seedlings from event -04	20	11	8.43	3.70E-03
T ₂ non-transgenic	0	6		
segregants of event -04				
T ₂ seedlings from event -06	46	11	39.42	3.41E-10
T ₂ non-transgenic	1	22		
segregants of event -06				
T ₃ seedlings from event -06-99	46	7	24.91	6.00E-07
T ₃ non-transgenic	2	10		
segregants of event -06-99				
T ₂ seedlings from event -08	53	11	34.2	4.97E-09
T ₂ non-transgenic	1	15		
segregants of event -08				
T ₃ seedlings from event -08-99	67	3	48.5	3.31E-12
T ₃ non-transgenic	0	6		
segregants of event -08-99				

Example 18

Characterization of the Low Light Tolerance of Seedlings from ME25698 Events

T₂ seedlings from events -01, -02, -04, -05, and -07 of ME25698 containing Ceres ANNOT ID no. 1373087 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01, -02, -04, -05, and -07 of ME25698 displayed a short hypocotyl under low light conditions in the T₂ generation, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 31).

TABLE 31

Plants	Short	Long	Chi-	p-value
	Hypocotyl	Hypocotyl	Square	
T ₂ seedlings from event -01	47	15	11.25	7.94E-04
T ₂ non-transgenic	6	12		
segregants of event -01				

TABLE 31-continued

Chi-square comparison of the hypocotyl length of ME25698 transgenic seedlings and non-transgenic segregants grown under low light irradiance (10 μmol/m ² /s) for seven days					
	Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
5	T ₂ seedlings from event -02	38	23	16.92	3.89E-05
10	T ₂ non-transgenic	1	16		
15	segregants of event -02				
20	T ₂ seedlings from event -04	42	13	30.2	3.90E-08
25	T ₂ non-transgenic	2	21		
30	segregants of event -04				
35	T ₂ seedlings from event -05	51	11	24.08	9.24E-07
40	T ₂ non-transgenic	3	13		
45	segregants of event -05				
50	T ₂ seedlings from event -07	43	6	11.88	5.66E-04
55	T ₂ non-transgenic	11	11		
60	segregants of event -07				

Example 19

Characterization of the Low Light Tolerance of Seedlings from ME25953 Events

T₂ seedlings from events -01 and -02 of ME25953 containing Ceres ANNOT ID no. 1440417 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01 and -02 of ME25953 displayed a short hypocotyl under low light conditions in the T₂ generation, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 32).

TABLE 32

Chi-square comparison of the hypocotyl length of ME25953 transgenic seedlings and non-transgenic segregants grown under low light irradiance (10 μmol/m ² /s) for seven days					
	Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
45	T ₂ seedlings from event -01	77	0	78	1.03E-18
50	T ₂ non-transgenic	0	1		
55	segregants of event -01				
60	T ₂ seedlings from event -02	46	4	57.48	3.42E-14
65	T ₂ non-transgenic	1	26		
70	segregants of event -02				

Example 20

Characterization of the Low Light Tolerance of Seedlings from ME25957 Events

T₂ seedlings from events -01 and -06 of ME25957 containing Ceres ANNOT ID no. 1505805 operably linked to a CaMV 35S promoter were grown under low light conditions and evaluated for hypocotyl length as described in Example 2. A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl, as described in Example 3.

Seedlings from events -01 and -06 of ME25957 displayed a short hypocotyl under low light conditions in the T₂ generation, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p≤0.05 (Table 33).

TABLE 33

Chi-square comparison of the hypocotyl length of ME25957 transgenic seedlings and non-transgenic segregants grown under low light irradiance ($10 \mu\text{mol}/\text{m}^2/\text{s}$) for seven days

Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event -01	48	4	56.6	5.33E-14
T ₂ non-transgenic segregants of event -01	0	21		
T ₂ seedlings from event -06	46	0	16.59	4.64E-05
T ₂ non-transgenic segregants of event -06	17	8		

Example 21

Determination of Functional Homolog and/or Ortholog Sequences

A subject sequence was considered a functional homolog or ortholog of a query sequence if the subject and query sequences encoded proteins having a similar function and/or activity. A process known as Reciprocal BLAST (Rivera et al., *Proc. Natl. Acad. Sci. USA*, 95:6239-6244 (1998)) was used to identify potential functional homolog and/or ortholog sequences from databases consisting of all available public and proprietary peptide sequences, including NR from NCBI and peptide translations from Ceres clones.

Before starting a Reciprocal BLAST process, a specific query polypeptide was searched against all peptides from its source species using BLAST in order to identify polypeptides having BLAST sequence identity of 80% or greater to the query polypeptide and an alignment length of 85% or greater along the shorter sequence in the alignment. The query polypeptide and any of the aforementioned identified polypeptides were designated as a cluster.

The BLASTP version 2.0 program from Washington University at Saint Louis, Mo., USA was used to determine BLAST sequence identity and E-value. The BLASTP version 2.0 program includes the following parameters: 1) an E-value cutoff of 1.0e-5; 2) a word size of 5; and 3) the -postsw option. The BLAST sequence identity was calculated based on the alignment of the first BLAST HSP (High-scoring Segment Pairs) of the identified potential functional homolog and/or ortholog sequence with a specific query polypeptide. The number of identically matched residues in the BLAST HSP alignment was divided by the HSP length, and then multiplied by 100 to get the BLAST sequence identity. The HSP length typically included gaps in the alignment, but in some cases gaps were excluded.

The main Reciprocal BLAST process consists of two rounds of BLAST searches; forward search and reverse search. In the forward search step, a query polypeptide sequence, "polypeptide A," from source species SA was BLASTed against all protein sequences from a species of interest. Top hits were determined using an E-value cutoff of 10^{-5} and a sequence identity cutoff of 35%. Among the top hits, the sequence having the lowest E-value was designated as the best hit, and considered a potential functional homolog or ortholog. Any other top hit that had a sequence identity of 80% or greater to the best hit or to the original query polypeptide was considered a potential functional homolog or ortholog as well. This process was repeated for all species of interest.

In the reverse search round, the top hits identified in the forward search from all species were BLASTed against all protein sequences from the source species SA. A top hit from the forward search that returned a polypeptide from the aforementioned cluster as its best hit was also considered as a potential functional homolog or ortholog.

Functional homologs and/or orthologs were identified by manual inspection of potential functional homolog and/or ortholog sequences. Representative functional homologs and/or orthologs for SEQ ID NO:88 are shown in FIG. 1.

Example 22

Generation of Hidden Markov Models

Hidden Markov Models (HMMs) were generated by the program HMMER 2.3.2 using groups of sequences as input that are homologous and/or orthologous to SEQ ID NO:88. To generate each HMM, the default HMMER 2.3.2 program parameters configured for glocal alignments were used. An HMM was generated using the sequences aligned in FIG. 1 as input. When fitted to the HMM, the sequences had the HMM bit scores listed in Table 34. Other homologous and/or orthologous sequences also were fitted to the HMM, and these sequences are listed in Table 34 along with their corresponding HMM bit scores.

TABLE 34

HMM bit scores of polypeptides that are homologous and/or orthologous to Ceres Clone 28780 (SEQ ID NO: 88)			
Designation	Species	SEQ ID NO:	HMM bit score
Ceres CLONE ID no. 28780	<i>Arabidopsis thaliana</i>	88	428.7
Ceres Clone 1073674	<i>Glycine max</i>	89	419
Ceres Clone 1118987	<i>Brassica napus</i>	90	418.4
Ceres ANNOT 1461298	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	92	435
Public GI 34907938	<i>Oryza sativa</i> subsp. <i>japonica</i>	93	419.6
Ceres Clone 1603237	<i>Parthenium argentatum</i>	94	345.8
Ceres ANNOT ID no. 1285138	<i>Arabidopsis thaliana</i>	100	391.8
Ceres ANNOT ID no. 1373087	<i>Oryza sativa</i>	104	419.6
Ceres ANNOT ID no. 1440417	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	106	431.3
Ceres ANNOT ID no. 1505805	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>	108	414.8
Ceres ANNOT ID no. 828846	<i>Arabidopsis thaliana</i>	110	422.5
Ceres ANNOT ID no. 832857	<i>Arabidopsis thaliana</i>	112	372.2
Ceres ANNOT ID no. 847799	<i>Arabidopsis thaliana</i>	114	391.8
Ceres ANNOT ID no. 856813	<i>Arabidopsis thaliana</i>	116	414.2
Ceres ANNOT ID no. 870022	<i>Arabidopsis thaliana</i>	118	390.3
Ceres CLONE ID no. 1025179	<i>Arabidopsis thaliana</i>	120	421.5
Ceres CLONE ID no. 1084747	<i>Brassica napus</i>	122	418.2
Ceres CLONE ID no. 1464359	<i>Zea mays</i>	124	408.4
Ceres CLONE ID no. 604111(a)	<i>Glycine max</i>	126	429.7
Ceres CLONE ID no. 964932	<i>Brassica napus</i>	128	427

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TABLE 34-continued

HMM bit scores of polypeptides that are homologous and/or orthologous to Ceres Clone 28780 (SEQ ID NO: 88)			
Designation	Species	SEQ ID NO:	HMM bit score
Ceres CLONE ID no. 1855399	<i>Gossypium hirsutum</i>	131	424
Ceres CLONE ID no. 1858527	<i>Panicum virgatum</i>	133	380.7
Ceres CLONE ID no. 1896482	Unknown	135	416.3
Ceres CLONE ID no. 1934537	<i>Gossypium hirsutum</i>	137	424.2
Ceres CLONE ID no. 1942084	<i>Gossypium hirsutum</i>	139	416.4
Ceres CLONE ID no. 1988960	<i>Panicum virgatum</i>	141	380.9
Public GI ID no. 92891522	<i>Medicago truncatula</i>	142	418.1

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TABLE 34-continued

HMM bit scores of polypeptides that are homologous and/or orthologous to Ceres Clone 28780 (SEQ ID NO: 88)			
Designation	Species	SEQ ID NO:	HMM bit score
Ceres CLONE ID no. 604111(b)	<i>Glycine max</i>	146	429.9

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

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tgaaagaaaa gggaaaaaaa gaaaaataa ataaaagata tactaccgac atgagttcca	780
aaaagcaaaa aaaaagatca agccgacaca gacacgcgta gagagcaaaa tgactttgac	840
gtcacaccac gaaaacagac gcttcatacg tgtccctta tctctctcag tctctctata	900
aacttagtga gaccctcctc tgTTTactc acaaataatgc aaactagaaa acaatcatca	960
ggaataaaagg gtttgattac ttctattgga aagaaaaaaa ttttggaaa aggctgcag	1020
gg	1022

<210> SEQ_ID NO 8
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0650

<400> SEQUENCE: 8	
catacttaat tctaaaaaaa caacacttat agtttataag cagctttat gataaaaatc	60
tttctgagtt atagctctgt taaaacttgc ttcaccccaa aaacggatgt ttcatttctt	120
atTTTTact tggagtatTTtattgtattt tgtaaaaaaa aatgttaaagt gggggatatc	180
atgaaaaaca acgtcacttt gtttggcac aataatacatt tgataaaata atggcgtcg	240
cgtgatttag tgatTTTTg ttttatcaac cacgtgtttc acttgtatgag tagtttat	300
agttAACATG attcggccac ttcaGATTG ggTTTGGCA catatgacat accgacatAG	360
aaggTTTAAAT ccacgtggGA aatGCCATA ttcaatgttt ggTTTCAAAG agagaatcat	420
ttctttatAT gatCTCAAAA gtatggAATT gaaatgACTA atgAGCACAT gcaattggTG	480
ctatCTTAAAC aaccgaACGT ctTGAATTt aatttGTTTt tcaccaAAAG tacctaAtGA	540
aaccCTTCA taaaaAAATA aaggtAACAA acaAAATTTt gtattggAAA aaacATTtt	600
tggaaatATAT aatttggtaa tagattATG agcaaaaaAG aaaaAGAAAAA gaaAGAAATAA	660
tgagcataat aaAGCCTTA cagtattact aattggGCCG agcagtTTG ggCTTGTat	720
catgtctagt aatCTTAAAC agacgataAA gttAACTGCAtttagtTGG ttcaGGTGA	780
ctacccaATC caaaaatacG cagattAGGT tcaccGTACC ggaacAAACC ggatttATCA	840
aaatCCTTAAG gttatacGAA atcAcGCTTt tccttcGATT tctccGCTt tctccACTtC	900
tcttCTCTGT tctatGCGAG acatTTTGTt ttatATGCAt acataataat aatacACTtC	960
tgtcaggatt ttgatttCtC tctttggTTt tctcggAAA	1000

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<210> SEQ ID NO 9
<211> LENGTH: 998
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0660

<400> SEQUENCE: 9

caagtcaagt tccaaatattc taaggagaaa taatagtata ctaaacatac attagagagg	60
ttaaacttct ttttgattt aagtgtgtat gcataggcta tttattctta agtataacta	120
ttaactgttag cttagatttat acaagaaata cataaaaact tatgcattgtg aggttagccat	180
gaatataacgt acatgttgca atcgattata catgttgtat ttggatttct ctatacatgt	240
tttaacttgt cattctctaa gtatatacat accattaata ctgtgggcat gagtttatga	300
taagactttt ctttggaga ccagtttgc tttccttcc acctatatattt gtctataaggc	360
ttcacggtag actagtttac aagtgtttt atatgttctaa aataaaatgt agatttccg	420
gaacggtagt atctgtttgc aaataaggac gtatataataa cagttatcaa tatattgtt	480
gttataaggc aataatataat tttctgagat attgcgtgtt aaaaaaaga aatattgtt	540
aagaaaaaaaaa aagatggtcg aaaaaggggga gtaggtgggg gcggtcggct tttgattgt	600
aataaaaagaa accacacgag tgacaccttccg attcgactca acgagtctac cgagctaa	660
cagattcaac tcgctcgagc ttctttttat gacaagttgg tttttttttt tttttttat	720
tttttcatct tcttgggttt ggttgggtca ctcttcaggc caggtgtgtaa aaaaagaaag	780
aaagaaaaaga gagattgttgc tttttttttt tttttttttt tttttttttt	840
acacaacaaa actccttcag atctgaaagg gttttttttt tttttttttt tttttttttt	900
tttattctcc gtcgtcggtt catgtctga ctctctggtc ttctcttctt cttcttctc	960
ttcttattttt tcttacttcg tcactgttgc gtctgaac	998

<210> SEQ ID NO 10
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0665

<400> SEQUENCE: 10

aaaaaggatggtaatggga cctattttcc ccaacatccc acatgcacac ttccctctcc	60
attctctcac atttattttct ttcattctaa tttatccatt ccgtgtgtaa catattcact	120
aataatctca tctcaactaac tcattcatttgc attgtgtat gtttatcttagt aattagtt	180
ttaacactgt gtctacatata gatttcctt tcattgtatg tgaacatgtt aactcaactaa	240
tcattttgtt ttttcgagtt aacatgagtc tccacttcgg tagactaaag taaagatagg	300
tttgagtata ataaatgttta aaatttgctt taaaatcaat atttataaat aagttttat	360
cataaggatgt ttttgcgtatgt tatattggac cttgtataaa cagactacag aagaaaat	420
tttatgagaa ctgttatgt tagagtggac ctcgtataaa ctaattatgtt gggctttac	480
cataaaactat ttatgaaaat tattatggcc cacaccacta taactaaagc ccacatattt	540
agcagccccag tttcattgttta agagacatgt tcgctctggaa actagaatattt tctgggtttt	600
gggttattttgtt tttcttatgtt gtagagaaat gatggtaacg attaaatgtt gtgttattaca	660
atttacaatgtt gtaagacgtt taatataattt acacacaattt ttgttgc tgtaacacgt	720

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tagtgtgtgt gatgatagaa tttcataaag cttaactac gaggggcaaa atgtaattc	780
taaatatgtt acagcagaaa aagatatgt tacataatat aaggattaaa acgtaataaa	840
taataaataa ggcgagttaa attaaaaccc tgtaaaacc ctagctgaa acacatgtat	900
aaaaacacct gcgagcgcag cttcatcgcc atcgccattc tctctctcat caaaagctt	960
tctccttgat ttccgattc tttagagtct taacgcaaag	1000

<210> SEQ ID NO 11
<211> LENGTH: 999
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0672

<400> SEQUENCE: 11

cagccgtaaa tcctccataa atttattttg caagtttgc tcattatata atgagcggaa	60
tttatgat aatcggtt aataatgtt tggtttgatc aaaatttggaa attaaaagta	120
ggtgagaact tgttatacag tgtagataag gtggatctt aatataaaaa taaaatttt	180
aagatgtatt taaaggcaga aagcataaaa ctttagataa aataatgtaa aatgtgtt	240
gcatcaatgt tgggatattt gcccacccga acttaatcaa tgtcggaaagc cattacttct	300
ctcccaaaag accttttcc ttccggagaac taggaacttc ctcactaccc ttccgttac	360
gtgaaagcca taaatttcat atattcataa aaatcagaaa atctaaaact gtttagtac	420
acctgtttt ggtatagact attgggtttt tgttacttcc taaactataat gatttcgtac	480
ttcattggat cttatagaga tgaatattcg taaaagata agttatctgg tggaaacgtt	540
ttcagtcat gttgggtcta gatttacata ctactatgaa acattttaag ataataatta	600
tcctagccaa ctatatgttc tatattatgg gccaagaaga tatagaacta aaagttcaga	660
atttacatg ataaatttact agtattttct aatacttggaa tgattactgt ttttagttt	720
tagaataat agtagcgtgt tggttaagat accatctatc cacatctata tttgtgtggg	780
ttacataaaa tgtacataat attatataca tatatatgtt tattttgtat aaagccatat	840
attactcctt gacctctgcc cccatttccct ttactataa ataggaatac tcatgatcct	900
ctaattcagc aatcaacacc aacgaacaca acctttccca aagccaataa taaaagaaca	960
aaagcttttta gtttcatcaa agacgaagct gccttagaa	999

<210> SEQ ID NO 12
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0676

<400> SEQUENCE: 12

aagatagtagc agtttcagt ttttgagaaa aaaagctgaa ctaaaactaa aatgtttttag	60
gacacaatatt ttagtttcaa tttagataattt caacagtttgg aacaattttt tttttttttt	120
tttgaagtca ttatattata caatgttttta aaacgcatttta agcattttagg cagccgacaa	180
acgccttatttgc tcttaactgtt aataggcgct tccactttagg ttcatattgc atatttacta	240
tatgtgtata gtgacaaaaa ccaatatttc ttatattttt gatgaaggta tagtagtgt	300
taaatgttca atataattaa gcattaaatgtt caaataaaat aaaattaatt tagttgataa	360
aaagataatc ttataaaaag atcgatgaat agatataatg gtttactgaa ttctatagct	420

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cttaccttgc acgactatgt cccaggaga ggaagtacct taactataat tctgaacata	480
attttgtcta ctgggtgag tattatatac cctaaaccct ttaataagaa aaagtataat	540
actggcgtaa cgtaataaat taacacaatc ataagttgtt gacaagcaaa aaaacataca	600
taattttttt aatgagatat attagttata gttcttatgt caaagtacaa ttatgcctac	660
caaaattaat taatgatttc aacaggaagt ctgagatgat gggccgacgt gtagttacgt	720
ttcttgaaatt gtgagatg gtatttata tactgaagaa aacattatTTT actaaataaa	780
tttcatttc acatcttctg taatcaatgc gggtagatga agaagttgtt aatacgatgg	840
ccaaccatat ggatctctt tttggcggtt ctatataatg taacctcgac tccaaaggca	900
ttacgtgact caataaaaatc aagtctttt tttcctttt tccaaaaaaaaaaaaaagtc	960
ttgtgtttctt cttaggttgg ttgagaatca ttccatttca	1000

<210> SEQ ID NO 13
<211> LENGTH: 998
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0678

<400> SEQUENCE: 13

aatttaatga aaccggccctt aaatttaggag ggattttgggt aagtggtaac acattcactg	60
gaaacatgtg aagaaaggag gatgtcaagt agctgaaaac tcagtatagt aaccaacggc	120
ttctcaccaa cctttcatta ataatttggt catccctata ttttttattca acattttgtt	180
tttcaatagc ttagagcacc ttaatacctt tcagtgtttt tttataaaaa aaacaaaaat	240
tgggattaat catcaatccc caaatgtaac gtttacttag attatgttca tttttctata	300
cacacaaatc atattttttt gtttaatct tcgaaaaacg agaggacatt aaataccct	360
aaaaaaaggag gggacattac taccaacgtt cattaacatg tttgatagca aacgatttat	420
tttggttcggtt ttgaaaaggg gaaagtaatg tgtaaattat gttaaagatTA ataaactttt	480
atgggtatagt aacattttcg aataataaga gagggaaaacg actcgccatt gtcggcaatt	540
tagaaccaat attagaaggg tttttttaga gaaaaaggac ttAAAAGTTT agagacctta	600
acaacaacattt atttagaaat agacatgctt aagttgacaa cagcgagttt attttctata	660
tcgaagaaaa atacgaactt tttcttaattt agatttcgaa tgcatgcaact atcgagaatc	720
gaccgtcaca agaaaaaaactt aatatacata ctgtacatata ctatattcaa tattgggtgg	780
gatgggttta atgtgtattt ataattcatg gataattca cacaataagg tccatgaaac	840
tagaagggtac caaaaataag cattaatgac tctttggccat ttatataatgattctctca	900
tagtaccatt ttattctccc aaacctatct tcttcttcct ctcttgatctc tctcgatctc	960
tctcttctac attgtttctt gaggtcaatc tattaaaa	998

<210> SEQ ID NO 14
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0683

<400> SEQUENCE: 14

gattgaatga tgagtgtgca cccttgtatt actaataaaaa aatttagcaaa cagttataag	60
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<210> SEQ ID NO 15
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0688
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acgtttcagag gcategctt tgtacaaatt gaagccccgtt tggtaaatat ttaaaataac 60
acaggaaaca ttcaaatgta ttattgtatgt tgcttaggtt tggaaatga tatgaaccat 120
atcgatatata ttactagatt ttctttatata gtttaaggg tagtggggct gacctatcat 180
tctgtttggc attaccaatc agactatccg agtatttcacc attcaggatt ccataactag 240
aaaaagaagg ggtttacatt ttctcataact gtataatttt ctactatccg agattttatc 300
gattacatta atctcatagt gattattctg atttataaaa aagttgacaa aataattaaa 360
accagtattt tataacaaga ttgtctctt cccatggcca ttatggac ctctgactta 420
tttaaatctt aattaacagc ataatactgt attaagctt tttaaatgaa acaaaataaa 480
agaaaaaaaaaag aacaaaacgaa aagagtggac cacatgcgtt tcaagaaagg ccggcggtt 540
ccgttaagggt gtgtcgaaact gtgattgggc cacgttaacg cggtatccaa aaaaaagaaaa 600
gggcacgtgt atagatcttag gaaaaaaaaaagaa agaatggacg gtttagattt tatctaggtt 660
ccagggaaatgggaaacgttccaca cccaaacggta cgtgtcggtt cctggccgtt gatgctgacg 720
gtcagcaact tcccccttatt catggcccccc tggccgtttaa ttacgtgtaa cccttccatg 780
cgaaaaatcaa accctttttt ttttttggtt ttttcttcaa cttttttttt taaaatcaaac 840
ctttttttttt taaaatcaca ttgcatttcc taacgctcaa caaaatctct ctctactaat 900
atctctctctt ctctctcttatttggaaag aagactataatcggagatt gttttttttt 960
gggtttgtct gtaaaatttggaa gaagttttgtt tagagatcaa 1000

<210> SEQ ID NO 16

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<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0695

<400> SEQUENCE: 16

aacatttct ttaacttact	cttaaatttt aatagtaagt	tgtatgcatgt tatgttgatc	60
cgtcttgc acaaatattt	ttttatggac gaattctttg	acagtaaatg gctatagtga	120
ctcagcttgg agcatcccg	atgaaaaca aagtgcagta	ttgtgtcggt gtcactacta	180
acgcacttc ctagaactat	cgcgcgtgtt tgacctatgc	aacacaccag atgtcatgaa	240
cgtatactta aatagaaaca	atgatataga caattggcta	tattctgtca tggaacgcaa	300
accggataac atgtcttata	gattcatcggtt acttgatcat	ggtttatgtct taatagacga	360
attctttgtt aacgattgg	taaaacggctt cacgttagag	catcctacta tgacttcaaa	420
attgataat attacatgga	aatcaacttta attttagtta	gaaggtagtt aatttagata	480
ttcttattta ataaataaaa	aaatagaaga aaaaaagatg	agaagagttt ttgtttataa	540
aataagaat atcttttatt	gtattttaaa aattaaacaa	atthaattta tattaaaatt	600
atctttgtt tattgttaag	gcaataatta ttttttgtt	ggaaattgtt aaaacaataa	660
tttagtatact gttaagtgg	ccttaataaa taagataacg	tgatttaaaa aagaacgaga	720
caggctaata tagtagagag	gaaaaaatac aatttaggcc	caataaagcc caatataagag	780
ttgtgctcaa acacaggct	tcgcagatt tcctatgc	ccgtgtgtca atcatgacgc	840
caagtgtcat tcaagaccgt	cacgtggcgt tgtttctaca	cataggcgat ccatacaat	900
cagtaacaaa cacgaaaaga	gcattcatat gtacgaaagt	agaaaagaag agactcttg	960
tgataaaaact aagtaagaaa	tagcataaaa gtaaaaggaa		1000

<210> SEQ ID NO 17
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0708

<400> SEQUENCE: 17

gtttccaaaa ctagtattct	ttatttgctc tattcattat	atttttatat ttgtaacgtc	60
ccgaccgtct ttatttaggtt	tcgacaatca ctcttcggaa	ggtcgtccat cctgaaat	120
ctctatccta aacatgttta	actataaaat tctctcgaaa	cttttgtaac gtatataacc	180
acataaaattc tcttaaactt	atttgcatac accattat	at ttctgaaatc gatatgttac	240
aatattatTT aatattttaga	ttacttttac tgaatcgaat	taaatatcaa atcgaacaa	300
atctaataccta	ccaaaaataa ttttgttata	acatttctt gcctagttt acctcatata	360
cattttagtt aaagaaaagaa	atcacaacaa ttcccataat	tcaataatata aatccacaaa	420
atcttggagt aagtaagaga	aataaaaaga tagtatctt	acataaacaa ttcaaagatg	480
ctctctcaca caattcacac	acacttacaa aacaaaagac	agaaacaatg ttttcatca	540
aatcaaaaga agttataaca	ctagtacaaa aaaagctcaa	attctaatacg taactcttt	600
tatTTcccaa ttacccaaag	attctctctc acttcacaaa	actagcttg agagtcgtgt	660
tccacaaaaat ccattaaagc	tgaaacgggtt ttgctcacca	ttcaaacaaa tacaaaattt	720
caaaaacccca aattataaca	aaataatata aaaattaaac	cgctaaaaag agtgaaccaa	780

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caaaaatcg cgaatgtgtg tgtaatgaga aaaccgaccc atcatccaa tcatcttc	840
ccgtgtca ctcttctct cccacgttcc ttctctttc cctttatggg ttttaacttc	900
tcttcttct tcttcttcaa tcttcagtt tcaaattcaa caacaattca cattttgatt	960
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<210> SEQ ID NO 18
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0710

<400> SEQUENCE: 18

tagtgccgt ggggagaggg aatggtgaaa ctttagtgt taagttatga ggaaaatgat	60
aaaaggataa aacaatcaaa tgcagcttga aacggccata acataaagta ccttatggg	120
gtgcgaatat ttttgtgttt ctttcactct tttattgtctt aaagctacga cacttgtctt	180
aatatattgt ttccgcaagt cacatgtatct actttttattt taacgtcttag aaacgccgag	240
atatatgtat attagtatata cacgtctatg caaattgtta gttcgtgttt ggccaaaaga	300
tatcgagaca tgtctgaaga accgagtcg gtttgagat atttcttcaa gcattactat	360
acaatagaaa aaggagacac gcgaatatga taatagcaaa aggcataaaa aggcgaaaat	420
taaagaaaaa cgtaaagtga tttggcctca atcaacggga acgtatctt attttagagg	480
ttcttcctttt acttttgaga cgagagagtt tgcgtcttgcgagctgctt tggttacta	540
aacattatca tattgaaaac caaaatacaa cggaggaata tttgtcacag tttcaacttc	600
acattgtttc cttaacgtttt aatcaacccctt gttcaaaattt tctatagtttta taatcatcat	660
tgtttacaaa attttcgttc aaagatgatt ttaaataaaa ttgtgaaaga aaacctttc	720
tgaataaagg attggatgat agtgtaaaaa gaaaaatatg aactggcataaaaaggag	780
tggccccgg aagattgtga aatgtgtcat ctaaaccagc cagacgttgttgcgtttct	840
cctctatccc ttgcgttttcc ccatttttttcc tttttttttcc tttttttttcc	900
cctacccatca tctctccat tttccatttttcc ccatatagac tcttttacaa tataaaaaac	960
ctatccaaaa gcgaagaagc caagcaaca tattataaaa	1000

<210> SEQ ID NO 19
<211> LENGTH: 1002
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0723

<400> SEQUENCE: 19

gtcataatctt atcaacacgt caacgatcaa aaccttttgc ctattaaattt caacggctta	60
gatcaaaacg aaacttaggtg ggtcccaactt ttaatatcgat ggctgcataa catttcctcg	120
ataactgaag ccgttgtgg ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc	180
agtacttcttgc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc	240
gagtttttttttgc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc	300
tttttttttttgc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc	360
tgtggtaat tttagtttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc	420

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tttggcttta	aaaatgttca	aatctgatga	tttgattgaa	gcttttttag	tgttggttg	480
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acttttgttc	tgcttggta	taaaatttg	gttgggttga	ttttgttaatt	atagtgtaat	600
tttgttagga	atgaacatgt	ttaataactc	tgttttrcga	tttgtcacac	attcgaatta	660
ttaatcgata	attnaactgta	aaattcatgg	ttctagatct	tgttgcac	agattattg	720
tttcgataat	tcatcaaata	tgttagtcctt	ttgctgattt	gcgactgtt	catttttct	780
caaaattgtt	ttttgttaag	tttatctaac	agttatcggt	gtcaaaagtc	tcttcattt	840
tgcaaaaatct	tctttttttt	tttgggttga	actttgtttt	ttaagctaca	catttagtct	900
gtaaaaatgc	atcgaggaac	agttgttta	gtagacttgc	atgttcttgt	aacttctatt	960
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<210> SEQ ID NO 20
<211> LENGTH: 1001
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0740

<400> SEQUENCE: 20

tgtggccact	aaagatttac	ccttaaccgg	gcccatataa	gcccacgtca	agtggcgctt	60
atacgtctc	cgtaagagag	ccaacatttgc	gtatgtatgt	ttgcaatttta	ttcttcaaga	120
caataaaattc	aaatataattt	caatattgtc	caaataatgt	gatgtacttc	agttgtgcac	180
atagaaactc	cactaaacca	acttttagat	agatgcattt	acaatatttgc	aacaatgtcg	240
cgaaggctca	atccatcacc	agattctaac	atttttaattt	ttatattttaa	ctatacatac	300
tctaattcagc	atgagtcaaa	cgtgtacaat	agcccaagca	tataataaga	ccaaagtcaa	360
actcaaataa	atgtctccaa	actcaaaact	tgaaaaagac	ctaatttattt	catggtagat	420
atgactttgt	cgacaagtaa	accaactaat	cctcgaagct	accttctttt	cccagttatt	480
atgtgtgatc	gatttataaa	tctcttcttc	taataacacc	tatatttttc	ttatgtatgt	540
aataaaatata	aaacttttaa	cttaaaaca	tatttatccg	aaatattgca	cttagatttgc	600
aaatagataa	ataatagttac	tatctaactg	atattgtaaaa	gacctaacac	ggaaaacagt	660
tttataaaaa	atccaaatgt	tggtaattt	tcttgatttgc	ttggggggaaa	cagaaaatgg	720
attaagatta	atcgaggatcg	tgtcaagcag	ctcgtaataa	actgttagcaa	gttgaactgag	780
taagcatcaa	cgtgtcatct	ccgtaaagcc	cattatttct	agtctcgccg	cgtttctct	840
tccacgttagc	acttcacttt	ttctcttcctt	ttgtttcctt	tggAACACAA	acgtttcttat	900
ttataggaat	attacgtcg	tccgtatcg	tgtcgaaaca	tagatccaaa	ttaaaagcgaa	960
cttacttaat	tacatatacg	tcgtttttt	ttcttcaaaa	aa		1001

<210> SEQ ID NO 21
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0743

<400> SEQUENCE: 21

tgcattggcc	cgatcgcccc	caaaatcaag	ctgagccgct	tcaaacttca	gctttgaaa	60
tcaccccaaa	actcatgtcc	tcttattcatt	ataactaaag	gatctttcat	tttatttaac	120

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tcatcgctt gcactaccca acccaaagg tccaaactata cccgaaggct tctaaaggc	180
caaagacttt tttttcgag ccagactatt caagccaaga aaagccaaac cccacaagcc	240
agtactttc aattccatat tataaactta tctgtcttg ttagtccca ctaaaaacaa	300
cagaattnaa tttaggttga gctaaaaccc ttgacaaaag tgtatagtcg tcgattcagt	360
agcacactca tcactcatca gatttgatag ttgacctaaa gtatgactac tccattcaa	420
ctaacaatg aaaataaaaag agacctaagg gtttagaggat tgaaactata ctctcaagtc	480
tttatcact aggctactac cagctagttt acttgatgaa tttaagcaag aaaacgtaga	540
atttatattc gagcagattt ttagctaaa aaagcttggg ttgaaatgtt cctttctcc	600
catataagca cgtcggttcc taaataactc ttcttagcgg agagtgtctt tccaataatt	660
taataaaaaat ggtgttgta tatcaaaaaa aaaagaaaaa agaaaactgat cgagatagaa	720
cgtttgcagt ttataaaaca attttaaaaa caaaaaaaaaat taaactcaat gtattttta	780
ttaattcaca aacaataata aatcatagga tcgaatattt acacgggtatc aaaacctact	840
cgccgcgtact atataaaaaat tgaagtcaaa tatcaaccgc aatttattaa ccagcaagac	900
aataattcat aaacttaata taaacataaa taaattaatg ttacacaacg atatatggtg	960
agggttattt otatcttctt cctctcaaaa cacatctcctt aaccttaagc tttagacggc	1020
ctgc	1024

<210> SEQ ID NO 22
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0758

<400> SEQUENCE: 22

agcttagccac atcagtggacc aaaaaagata attaacaac caaataaaat aacaaatttt	60
gatcatttgg aataaaatttt ataaaaggaa cgaaagcgcc ttctcacggg tcccatccat	120
tgaatataat tctcttttt tgctctatata aataataacg cgtactaattt tttttttttat	180
attattacaa agtcgatatt tgattttttt gtgaacgttg atatattttt tttttttttat	240
gatgacaaaaaa aaagtcataaaat aaagtaacgt gtgaacatag cattaacaaa atacaacat	300
aatatataac caaatatataatg aaaaataggat aaaaatctcat tgaatagatc ttcttctatt	360
caaatatata aatattttttt tgctctatataa attaacagag cattcacattt atctaaaata	420
atagtaaaat caaaaataaaa ctaaataaaa ataaactctgg ttttataacg attgatttttta	480
aatattttttt ttgttgtttaa agagatcattt atatatgtctt gtaatattttt tataactgtttt	540
tacatgatattttt ttagttttaa tagcgtaattt aactaagata agaaattaac taaaatgtata	600
ttcttgattttt tattttttttt ttgttgtttaa agagatcattt atatatgtctt gtaatattttt tataactgtttt	660
caaaaacggta taataaaactc accattactg gaaaatgtttt gcatttgactt caataagtaa	720
cttattataat gttactgata taatgcatag ttttggaaatttt cttaaataaa ttatgggtt	780
tttcgtatggaa aatatgaaag gagagaaattt tattttgttc actttatataat atatacatcg	840
taatcattttt ttcgtgtataa atttctcttc ccattccattt atttctcagt atctctctt	900
ctttcccttaa cttttttttttt gcttttaaac cttcaattttt ctcataaaacc aaatataaa	960
tatcaaaaaca aacaaacaaa aaatcagaat tccccctaaataa	1000

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<210> SEQ_ID NO 23
<211> LENGTH: 921
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0829

<400> SEQUENCE: 23

aaagtttga attattggga atcaatttcg aagtttgtta attcttggg ggctaataagg	60
atattttatt ttcttggtt cgtctattgt tgttttcta tttatggtg ggcttttaga	120
actctggaca ggcggatgtc atatgtttc ccttctcctt atattttca tttttcattt	180
tgttaaatta atgcataata tccaaaaca atttaaattt ttgaaggaac ccttttagtt	240
cggctccgaa gctttcacaa gtgagaatgt gagatcaaag aaggcaaatg gaggattta	300
aaagttaaaa tcatcttta tctgaaaag ttgacaattt ttttgtatca aatctaaatc	360
atcaaactct cttaaactac aagagcataa caacctctat gtaatccatg aaataatctg	420
cttgaaggac ataacataaa tcattatggc tagagtactt aacctcaatc aaatctctt	480
aactcttagt cccttacaat ggtatcgtaa aacattatgc attagggatt gttgtccatg	540
aaaaataaaaa taaaatccc cacagaccaa ctaccattt aacttaaaaa taagcttcgt	600
ccgcgcacgaa ttgtttcca tcctaaaaat agaatgggt aatctgctaa tggtttagtt	660
ccattaaacctt gcaagttcta ttgaaagctt aaatgtcaat aaagatattt aaattcggag	720
tcaaaagaca aatgaatcaa aagcaacaag acaagtcagc tccattctc actaccatc	780
ttttacaata aatcatctt ctttcacaat atttcaactt actctcatg cccttagct	840
ttgttataga gccaacacta cagagagact cacacacttg tttcaataat taaatctgaa	900
tttggctctt cttataaact a	921

<210> SEQ_ID NO 24
<211> LENGTH: 763
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0837

<400> SEQUENCE: 24

aactacaagg gagacataat atcaccatct ggttcctgtt atcatctgaa gatttctgt	60
tttaccttcc agtgataaaa tgatccttat aatacatata gatatattaa attgctgtat	120
tttaagatta tagatata aggtacatga gagtgtttat taaaaaaaat tcacttgaa	180
ttcatgtttt gtgatacgat agatggaaat ccatttggaa aaagaagaat catctgtct	240
tatgtctcaa atttgactt cattcaattt tcttcttgct ttttaagaaa gcttcacaa	300
tctaactgtt cgatgtgaaa actgagattc gagtaagaaa atgtgaactg tgttatactg	360
tttttaattt agataatttta gattgcactc agataaatttta ataacattcc tcgaataactt	420
ttatgtgatt ggatataatctg ccaaccaacc aataaaactgc tatgtttaaa	480
caaaatataat aaatttagtat atgtttactc aagaataaaag aagatagaaa agaaaattct	540
atatgagcta aatttgcgtt aggaggcatc ggacgtgggt accagacctt tccaaagcaca	600
cggatgtgc ttatccatgt catgctaaca tacaccattt ggatcataca aaatccaaat	660
caaaatctat tttaaaaatc ttggcacac gtcttggaaa aacacctctc atactatagc	720
tacggaaatc tcaatttcaa ggttgtctt aaagctaaacg att	763

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<210> SEQ ID NO 25
<211> LENGTH: 751
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0838

<400> SEQUENCE: 25

atactggat gcttaagggtt gaagccaaga tctctgtctt acccaagtaa ccactttcta	60
ttagaaggga tcaacactaa gaatatggag atttaagcct aagggctaag gcggttctca	120
acaatacatg atgtgaatac aatcacagac gatttactga ggtttgtga taagatcttg	180
atcagtcctgcatcatctg ttcaacaatc tcaatcttg actgtttgct ttccggagcca	240
taaacagagg aatcccttat tccctgttat aggagcaata caccaagtat tatttccatg	300
gtgaaattc tcttatggaa acctaattgt tccattgaag ctgtaaaatc gaatctggtg	360
aatattctcg agcaaagccg catgctaatt atgtcaattc agaagagttt gattaggaga	420
ctcgaagcga gtttgcgtat ctttcttgcgt gttcaactcc gattgttaagg gtataattga	480
cttttcattgtt attacggctc caccacctga cactaaggca ctctttgtcc atctcggtgg	540
tatcatcgga ttccggatgggt aaaaataaaa agagcagagg aaacttgttcaatcgcaag	600
cttctcagggtt gccaacgtcac tccattacgt gtcatcttca cacaccatct cgctcaaaac	660
cgtatctcatttttcaaacct taaaggcaga agcaactgat taagtttaca ctcttgagaa	720
gctctcgatt aagcttgcac ttggaggatc a	751

<210> SEQ ID NO 26
<211> LENGTH: 669
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PT0848

<400> SEQUENCE: 26

tctctttaaa tcagtttaact aaccgtttat atatttacga taagggttga agagattatt	60
gataaaaataa tacatttcat aatcccgcgt tcaaccgttt aaagtaacat ttaagttgac	120
tatatactaat ttttttcca ttaaatatgg agctggtaaa cttttatcaac ttctaaaaag	180
tgtaacaaca aaaatttaggt caatcacaat tctgttttt ttatttattt ggattgactt	240
ccaaattgcaaa atagtcttag tgatcaccat tatcatacat atatacatca agtaggttc	300
atcatgatat accacaaagt atttgacaag ccatatggtt ttggatcaaa aagtcggtcc	360
aaaattaatgtt ttttatgtgc aagaaccgac ccattgtaca cacgtgttaa catcttcaag	420
actttcatct ctattttct tttggtcatt aagataccca ttgatccaa tctgttacat	480
tcccacatc ttttttaatttttactatcc actccaaattt aaacacaacc gatgatTTA	540
ataatttgaa gctttaaaa atatttcaaa acaagcctct ttgtgtttgt ctatataat	600
acacgtataa agaagggtgaa tgaatctcac agcttacttg ttcttaaggct tccaataacg	660
aaaacacgtaa	669

<210> SEQ ID NO 27
<211> LENGTH: 702
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<223> OTHER INFORMATION: Ceres Promoter PT0863

<400> SEQUENCE: 27

cgggaaacga caatctgatc tcttagtccag tcgattggcc cgatcgcccg attataaact	60
tacatgagac aagtataaat aattattata aacttattaa gtttaagatc aaggctttg	120
tgcaatgtat caatgaatgt tagatgtatc atgatgaaag caatgtttt aacacataca	180
tagtcattga tcggaatgtg tggttattaga aatgcattgc taagccgata gggttatcta	240
tgttttgtct tggacattat agccaaattt cgaatctaata tcttccaata tatattttt	300
ttttttgtct tagggccact actagtattt cttatcaattt ttaagagctc atgaaaatgc	360
aacaatata tagttgcaaa tccttgttcc aagagaaatc aaaggccac ttgtgaattt	420
aataataata atatggcaa ataacccttc actaaaccat accaacaaaaa ccacacagat	480
ttggcaaaga cataaccctt gggagacgtg aaaaggctca aaatttgaca attgtcctt	540
caaattcgct cattagtgcata ttgtgagat ttgttgcata ccaaattccaa ttcataactc	600
acactcgctt caaattcgaa aaggcctgcata gggccagtgc actgggatcc aacaatgtcc	660
tccgactcgtaa ccaagatcaa gaggaagcgg aaccgcacccg cg	702

<210> SEQ ID NO 28

<211> LENGTH: 435

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter PT0879

<400> SEQUENCE: 28

ttcttaggaag actggtaaag ctaagctgtt tctgtttttt gttttgtac tttacttttt	60
gtttgttagt gggactggg tttattggc cttgaagttt ataaaagatg aataaaagac	120
atatcgctt aagccatat gagaagcaga agacaaaaac ctccaaactt gggcataaat	180
tttgattata gttaaaagtc cagacccat tttgcacccg gtttagtttac gattttaagg	240
catgacacctt gcctaatatg tttattacag aaaataaaga gaatcagctt ggtgtccctt	300
atggAACACA ttaacaaactt ccaacgacac tacgtgtctt cgtgactctt actatatacca	360
aaaacctata gctaaagctg aattttccat gattgtata gtcccaacca aaaaaatact	420
gaagaaggca taagc	435

<210> SEQ ID NO 29

<211> LENGTH: 397

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter PT0886

<400> SEQUENCE: 29

agtgtatTTT aaaacgacat tgaagaatta atatattttt ttttaattttt agtttttat	60
agtacaaata ttaaaaacaaa caatcctacc atatcataac atttgtaaat aacattttaa	120
gtttttgtttt gagttttat taatTTCTA tgacaaaaaa atgaagtcaa tagactaagt	180
gaatcatata gtataaataa acacaattta aatagttca aataaattta gaaagaataa	240
aacaaataga aatcagaagg tgtctgttcc ctcctcgcaaa catacgatca aagagaacaa	300
acttgaccct ttacattgtt caagagctca tctcttccctt ctacaaaaat ggccgcacgt	360
ctccaaacccctt ctcccaactc cttttccgc catcatc	397

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<210> SEQ ID NO 30
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0007

<400> SEQUENCE: 30

agcagaacaa ctatatttat	tgtgtcacat aaatctgaga	tcatttataa ccaccaaaga	60
acctatacac agtaaatgac	aaatgtatct ccccttatct	ctattgccca tatgttagatg	120
ctaaagtaag atttctcttt	tttttaatgt actttttttt	gtataaagta tattccataa	180
aaaaaaaggaa aagcttgg	ttt atggatcaat tgaccccaa	aaaagttttt agatcaaagc	240
ccaatataaa aaaaaaacac	agtagtgaca caaaggaact	taaataaacc atgaattgat	300
ctataaacag tagagatcga	taaggcgaac atttccatg	tgaagtgtct tcattcatct	360
ataatatttt tgacatccaa	taattccctc tataatatca	ttcacataat tgatagaaac	420
attatgttag aattgtccac	atcatttgag ctgtaatata	ttctgtttt acaaattata	480
tggtagttgc ttaatctt	at gtccatctc ttctatgcat	cgtttcgcg cctagttgtc	540
cagtccattt caactaccta	cctcttaattc ttatcttaaa	acaacatttt ttaatttaag	600
tattatgctc aaagactaac	tagatagaaa accgttttaa	aacattaaac gaattaaaag	660
tcttacatgg aaaatgttagg	tttataaacc acgagttatg	attgacaata aaaaaaatgc	720
aaatcatcaa taaaaagaga	cttgagtgcg actctatatc	aaccattgca attaaaatta	780
tctatcacaa aaattttaga	cagattaagt taatttatgc	taaatttact aatttattt	840
ctataattag taattaacta	tatttattnn tttacacatt	ttctgataat ttagaaattn	900
gcatgaataa caaatataag	atttggaaa ttagtagcaa	attnaattaa taattattn	960
tgcctaaatg aaccaaacta	taaaacctcc acatacacca	gtcatcaaat ttacagagac	1020
aaca			1024

<210> SEQ ID NO 31
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0008

<400> SEQUENCE: 31

ctcgagagat gaagtcttag	taatgtttga acaaacaata	atcacgtttt ccatcaaatt	60
cgagcattta aagtttat	tactacatgc cccaaatgaa	taccgtccat ctcatccgaa	120
aatatttctg	aaattgcgtc aagacaacaa	tgttgtcata aattcgatca	180
acaaatctct	catcaatctt acaaacttct	cacactaac agaggtacat	240
aaagacaaaa	gttgcgaaca gctggcttct	caactcgagt tgggtgtcag	300
cactaactac	aaatgggtac ttcaaataatt	ggtggctagc ttacagtgtat	360
ataaaaaccc	atgaaaaagc tgcattaatt	gttccaagtg aaccctgagg	420
gtctttgctt	tagtgtgatc attaaacca	atctctaaat tcctaatttg tactaacatt	480
tggAACGTAT	tccctactct tccctctgt	ccaaactccccaaaataagat tagtttagatt	540
tctataacta	atatacatgt atactccaa	aaacagtaaa accatattaa taaagctaat	600

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tttgcata	tttatttcgg	taaacccgac	gttcaagttg	ggggaaaaaa	agacaaaacgg	660
tctaaagtca	tccaaagaca	aaaaaccaaa	gacaaggta	gagagacgag	accaatcaca	720
acattgttcc	gttagattgcg	tgacatcatc	cttgacggct	actttcattt	gtgttattt	780
tggataaaac	gcacgtgtt	aattcacgaa	ccttcatacg	aataagaat	ttccattact	840
ttcatatttt	caactttttt	tattacccat	tacatgcta	aatattaat	tcacaagttt	900
tttgtcaaat	tcaatatttt	ccaggttcat	gaaccctttt	tatctcaatc	tactctataaa	960
tatctccctta	taaattacaa	caaaaacctt	ttatttttca			1000

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<210> SEQ ID NO 32
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0028
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<400> SEQUENCE: 32

gtcagtgaag tcgattggta gtacttgaaa cacttggttg gtttcatgta tttggctat 60
atataaacaa acatcgtaat tatatacggta ttttttcgg aattttacgc catabctgta 120
agtatataata acatgcatgt cgaaaaaaa ttccatatgtt gaacgatcca cgtaagtgt 180
actactccta caatattgca tgagagagat atgtattttt aaatttttatt ttgaagaaga 240
aataagagg aagggttactt gggtggatcg atgtgaaaaac aaaagaagaa aaaggcggaaac 300
ccactaaggcc attacatgtat atcgacccccc ttatctttt cctcttttatt ttatctttct 360
catcttctttt ttgtcaggac tttttctac ttaatgaaac ctccaaacta tctaactaat 420
acactccccat gtagaataaa gaaaattata taagatattt ttgatattttt gtaactagaa 480
aatatatttg ctctgttaattt ttcgttaagt taaatcaaca ttttaagta gaaacaataa 540
ttactgcaaa aagtaggatc attatcttttgc tccaaaatct cagttagcta tagggttgta 600
gtaaaaacaa aacacattct tgatttggcc caaaaaataa agagagagaa gaatattgtt 660
caaaagtgg ctcttcctc tctaattatgt ttttcaactaa acccaatttag attcaaacag 720
tctacaaagt cccaaaagata aacatgggac aacaattcgta tgcaaaaaat cctctttca 780
tgtctttttt ttattctcta gtctttaaa ttactaataaa aactctcacaat atccacccaaa 840
cccatctctc acaactcacc ttcatctaga tttacccact cccaccgaga aacacaagaa 900
aaaaaatata catataataaa tatacagaac aacacatgtat gctgatgcaa tatacacaac 960
aaagtattaa atcttagata ttgtgggtct ccctttcttca tattcatattt cttattcatt 1020
aaaa

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<210> SEQ ID NO 33
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Ceres Promoter YP0029
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<400> SEQUENCE: 33  
  
ccgttcgagt atttgaaaat ttcgggtaca cccgcctaaa taggcggacc ttatctagta 60  
  
tatataataca tttagaactat attgtttact ttttagttaa tttaggctat gtcatgacat 120  
  
tgacataaaat ctacctgtta tttatcacgt gtaattcgtg taaagtgtaa actagaaagt 180  
  
tcaaataacgt atttgtttt gttcttttat ataggattgt catagttgta aatctacaat 240
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tttataacac atgaataagt acacaagcaa tgtaattgga tttaattgct aaactctta	300
catggtaat ctaaatttga taagaaatac gtcacatatt actaagactg atatgtttt	360
tgttgtcac aattattttt gttaaattga cgaaaacaat tccaaaaact caaatgtaca	420
aaatcataca gtctcacaaa catctcatag agaaagatat aaatctccc tatgggaacg	480
ataacacgag gtcgaaatac tattcgtaaa actaaaacgc cttagttata aatcgtagt	540
tgttaaccgcg gtcgagaata catacagatc cacgaaacta ctactacaca tgctgctgaa	600
ttggaatttg gaaaagacca tcttcttag gaagagctca cccaatgagt gacaaagggtg	660
tccgtggctt gtttctacc catatgtata catcaaattgg tagtttattt aacggttgg	720
tttgagaaaa gtaagacttt ggcttagtagc taggttcgta tataataaac tcttttgaga	780
aagttcatca ctggtgaaaa atgttaaacc ggtttttctt catttttcc gccatgttaa	840
ccacccggtt aaaaagaccc taacacattg aaagattaat aagggtatata ttgttaattac	900
ggtttgcgtt caatttttaa ttattttttt aatttagagaa aatagagaag ccctatcaat	960
gtacatggta tataatataaa aggcaaaacc ctagaaaacg atactattcg actcagccgt	1020
cctt	1024

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<210> SEQ ID NO 34
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0050
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<400> SEQUENCE: 34
aatctgatct ctagtccagt cgattggta c ttgaggaaa catcatattt ttaaaccttg 60
tctcagtaa g ctaacacaca ccccttgc ttacttatcc atgtttatcc acaagaatgc 120
agttggattt agatatttc ttctttgtt aaatcaggcc tcaagggtt catgtggct 180
gcaaaaaaaat tcccaaaaat aaagatagtg acatctgaaa tcgataatgg attagacgaa 240
gagtttcgtt ttattcctt gtatggcg gtttggggac agatatttt gcacagacga 300
ggacttaggcc actgtggtcc tgcagcatta ggtgtccctt ccatgtccctg cattacattt 360
tattgtgga ttcatcaccc tatctactac aacggctaca caaactatga agagtttgt 420
ttactaataa atgccaagt gagggttcga tcgaaccgg gacacgttt tcagtttacc 480
atataagaatt atcccttggaa cccttgatac tccatagaac atcaccacct ctgttgtcat 540
ctcaggaatc cagggtcaaa cctagtctct ctctccctag tggggaggtat atggccactg 600
ggccaaatgat gacaaaaatgc aaaaaaaaaata aaatacattt gggttcattt tctaaaaat 660
ctcttgtgtt tgtaagttt ggttgcacac tcgtgtggtt gaagtgtgt tgagaggtac 720
tataacaatac actctgctt tggttgtac ctatctttt ctcttcttcca cataatccaag 780
actttggggta aaaaagctgag atcattggtt gccattggt tgggttggaa caatcaccac 840
tttgctttat ccgagggttga taaaatttcc cgggttcc ttctgacacg tatgacaaat 900
tctaataatgtt tattctcgat agatattacc tataatattctt caatagttgc aggtacttaa 960
gggtttgtct tggcatccctc gtcctttca gcaaaaactcg tctctttgc actccaaaaa 1020
qcaa 1024

<210> SEQ ID NO 35
<211> LENGTH: 999

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<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0086

<400> SEQUENCE: 35

cttacccccc	aacaatgaac	aggtttttag	aggttagttg	atgattcctg	cacatgttat	60
cttgggttca	ggcttaattt	tccaggtaaa	gcattatgag	atacttttat	atcttttaca	120
tactttttag	ataatgcaca	agaacttcat	aactatatgc	tttagtttct	gcatttgaca	180
ctgccaaattt	cattaatctc	taatatctt	gttgttgc	tttgttagac	atgggtacta	240
aaaaaaagcaa	actacaccaa	ggtaaaatac	tttgtacaa	acataaactc	gttacacgg	300
aacatcaatg	gagtgtatat	ctaacggagt	gtagaaacat	ttgattatg	caggaagcta	360
tctcaggata	ttatcggtt	atatggaatc	tcttctacgc	agagtatctg	ttattccct	420
tctcttagct	ttcaatttca	tttgtgaggat	atgcagttt	ctttgtatat	cattttctt	480
cttccttgc	gtttggagtc	aaaatcggtt	ccttcatgt	catacatcaa	ggatatgtcc	540
ttctgaattt	ttatatctt	caataaaaat	gcttgtacca	attgaaacac	cagctttt	600
agttctatga	tcactgactt	ggttctaacc	aaaaaaaaaa	aatgtttaa	tttacatatc	660
taaaagttag	tttagggaaa	cctaaacagt	aaaatatttgc	tatattatc	gaatttca	720
catcataaaa	actttaatttgc	caccataaaa	ttttgttttgc	ctattaatga	tgtaatttgc	780
gttaacttgc	ataaaaataa	tattccgtaa	gttaaccggc	taaaaccacg	tataaaccag	840
ggAACCTGTT	aaaccgggtt	tttactggat	aaagaaatga	aagcccatgt	agacagctcc	900
attagagccc	aaaccctaaa	tttctcatct	atataaaagg	agtgacat	gggttttgc	960
tctgtttttt	aaagtttctc	gttttcttgc	ccgttttctc			999

<210> SEQ_ID NO 36
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0088

<400> SEQUENCE: 36

tgcattggga	ttactacttc	atcttagtaag	gttctgaaaa	cgtttgttgc	tgataaggaa	60
gattcgtctc	aggatttttt	tgttgatctt	caaggtttgc	gattgtgc	cttatacatg	120
tgctgaaact	gtgggttttgc	tttattgaaa	acaaaaaaaaaa	agtctcttgc	gtagtttcat	180
tgtactaaat	agaaaaacaag	aaacgttttt	ttctttaatc	ttctacatgc	ataatatgg	240
atcaaaaggat	tgtttctgc	agacacaaca	caaacatact	tataactgtt	tacttctact	300
aagtactaac	tacataccca	tacacacact	tgcacctaga	ctttacttct	agacatcatt	360
acccttaaggt	agaaccaagc	ttacaagcaa	gttttaccga	caactttac	attacaactc	420
tagtctgttag	tctttaacgt	agacttacta	actagtcatt	agtggttaa	ttttttaaat	480
tttcatccat	atgtttttgt	tgttagatata	aactaaagtc	ggtcacat	aataattgtc	540
attatgtccg	cgtaaaaagt	aattcagct	ttggacattt	atgaaatgt	agattttctc	600
tctcatttcc	ccgtgcgtga	agacatgc	ttgggtttct	gtaataatca	acaaatccaa	660
accccttttc	gatctttatt	ttggacatttgc	tagagacaaa	atttcttat	agtcttttc	720
ctaatttgat	accatgttttgc	caaatttact	cactggtttgc	actaactatc		780

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cacttattta tgattttacc attaggcgctc agctagccct agtcaaattt gtaaacaagc	840
caagctatct acataaaatcg agatgtcatt aacgttaatc gtcgttaatt cgaatttgaa	900
aacatagata gcttagcag tacaatgggc aatggtaaga agaatagcaa aaggccaaat	960
atttggtttgc cagaaattaa agccttaaaa aaaagcccac agatatttgt caaagaaccc	1020
taat	1024

<210> SEQ ID NO 37
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0092

<400> SEQUENCE: 37

aaagattgag ttgagagaga tggtgagac gcagaacaga caaagggagt ttaccatata	60
gtgctctaaa gggcaatgag attgcagtga tggctatc cggggatca tcgcaggta	120
tcccttccca tgagcaacaa tcaatggatg ggttccaatt cagaggagaa acagaagaag	180
aaacgttcc agagaaccac agtagggatt ctgcgcattc cgagttgcag agagectctg	240
aaactgoat agaaaggaca ctgatgaaaa gaacacactg aaggagtatg ccaatcatgt	300
gaaaactcg agcttgattt ggttgggtgg ttgtatgaaatg tctcacaaaa cctttggctt	360
tgaatctccc ctcattagtc atggtgagaa caagaacaag acgagaaaca gacaaagaag	420
atgaaaaaac ttgttgccca gtgttgacta agggggata gccccagaca taacaaaatt	480
agacttgcg tacatcttta atatttttt atctgtttct ttgtcctgac gcttcattta	540
tccctgtgtat caatttctc ataccattgg tccatcgta atcctttttt aatttcattt	600
tctacgtaac atgagaggag accaagtctt atgagaacag ttgacgtaac agtgggttgg	660
aagtttaattt aaaaagagga agcttagtgag agtgaccgtt aggttagagaa gtgagatctt	720
taaccactct tctttctctc tctctctgtt ttttcgtcg tctttcacat ctactgtcg	780
caaactctct tatgtttcca ataatggta taccattga gacttgcagg agaatctcct	840
cttctccaca ctctatcaac tggtcagcca tggaaatggtc gtttcagttt caatattcct	900
ggattttttt taaggattcc tggttctttt ctgttccctgg tatattctta acgacgaaat	960
tagtatcgaa tcctggtaat acatttgaa gcttttaagt accattgcac tgggatccaa	1020
caat	1024

<210> SEQ ID NO 38
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0096

<400> SEQUENCE: 38

gaggttcagtg agtcgattgg tgcaaaattt aaaaattgaa gggtgaaaca aatttaaaga	60
taatatctat taaatcctct aatttaaaaa attagcaaa aattgtattt tcttatggat	120
ctgttagttc acacgtatct taatttagtac caaatcatat ctaatgatta gtgataaaac	180
tagtttagata tctatatgtt tctttaccat ttaacttgaa tctttttctt tttttttacg	240
taaacaacctt gaatcctcg ttaatacata aatttaaagc atttttttttttaattctatt	300
gatcggtata tattttactat aagtttttagc tcatatgcaa tttcaaattttatgatatgttttta	360

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aattttgtct aggtgtgata gttgtatctt taacataaaat cttatagcaa aattatactt      420
gatattctaa atttatctat ttgctcttgc gAACCTCATA tttagtctaga gAAACCTTGA      480
aatcctttca attagttgta tgtccaaatac atttttacta acatTTTATTA gtcttttAA      540
ttaagattat tgTTAGAAAA AAAAGATTt tttAAAATA AATAATATGT tttAGATACA      600
atgtgagttt ggCTTCTTAT atTTTAAAAA AtAAATTtAt ttcataCTTA AAAAATAGTT      660
ggAAATTCAA TTtATTTGGC tgaatACCAT AAATATGTC AATTGAAACt TTATACCCAT      720
tgactatTTG gtGTTAGAAA CCCTTAACA AAAAAAAct ATTTGGTGT AGATATCAA      780
ataaaaaaaAG ttAAACCATT ggTTTCTTAT AtTGAATTGG AtATTGTTAC AtGTATTTAA      840
gtTTTTTGG ttAAATTTG aaACGTTGAT AgAAACTATT aAgTTAAGT ttGTTAGTAT      900
atTTATTTGT ggAAAATTTA AtTGCCTTA AATATAACGT CaACTTTTt TGGTTTTT      960
tgagaagtta cgTTGTGATT ttGATTTCt AtATAAAAGT tagATTACGT CATTtTTAA      1020

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<210> SEQ ID NO 39
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0097

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<400> SEQUENCE: 39
ttcatcttta tatttaagAG ttAAAAAAct gcaacttttG ttttCTTC actaAGtctt      60
atggccacAG ttaattttAA gcAGatgAAA ggtggtccAA tggAAAAGGA gaatgtgatt      120
gggCTAGTTG ggAGAGTTCT gatgtctAGt gttgggtaca cgtgtccgTC agttacacat      180
agcattaaATt cagacggcat gtcatttttC aaatctAGt cacatAGtAC gactaATAGC      240
tgataAAAtt atgattatac agcatatgAA ttatGAATTt AAAAaaaAAA AAAAATTGAA      300
aatgttAAGG agatgtATA ttttacAAAAtt catcgcaA tgctttctAC taatttgcTA      360
agtggcttC tccAGTTAGt ctTgtcgatt ccaAGCGATA ttattAAAtC ttGAAGCAtC      420
gctcaAAAGCA ttatAGCTt agataACCA AtTgttAttA AAAACACCTA gtGAAAtTTt      480
taaattttAA CAATTtGAt atctttgtAA tatctaAtAC tacttttCT gtgtctAAA      540
ggattaAtt tcaAAAttt cacacatAtt AAAAaaaAAA AAAAAttACT agctAAACAA      600
tttcaAttA tcataAAAcA atAgtaAttA aAtAAtttt ttttAtttC AAAAtAGtCC      660
ttcaAGttaA caatttCAtt tagtAttAtA atcaAcAAAAttA aAAGtGgAA      720
aAttaAtCtT tGtGGAACAA AAAAAtCtAG AAAtCAtttt ttagAAttAG agAGAGGtt      780
gataAAAAtt AAtAAAtttt AAtAGAGAGA ggtAGtACAt ActAAACGAt gtGAtACtAC      840
tattgacAAA atcttAAAtC tcAGTTAGt agAAtAAAct agAAGGAtG aAtGAAGtAA      900
atgcGAAtCC AactActAAc AAACCCtACT tagtCatCat AttttCCtAt AtGAAAtCC      960
tatataAAAcc catcatcatC tcccActttt ttcAtAtCCa                                1000

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<210> SEQ ID NO 40
<211> LENGTH: 1004
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0101

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<400> SEQUENCE: 40
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ttctcgttct ctagaatatt gctggaccgg attaggtcaa tattattggg ccagattaga	60
tattgaatt tcgacgttgc ttacgttacg ttatatatgg ttaagaatt aaacatctcg	120
acttagtctt aattaagaaa acattgcctt aaattctctg gtctgegacc gtttttttga	180
ccgttaaccc ctaattaaag aaacaaaata attatagaaa gagcactgaa atgtgattat	240
ttAACAGTA CTCTTATGAG AAAATTCTGA CTTTTTAGT TTTTTTTGT ACAAACTCT	300
aagaaaaaca ctactactaa ttaagaaacg tttcaaaacaa ttttattttc gttggctcat	360
aatcttctt tctcggtccg ggactaaccg ttggcaaaaa aaaaaaaaaa gttgacaata	420
attattaaag cgtaaatcat acctctcaa taAAAACCTTG aatttggaaa caaagacaac	480
taaaaaactc gaatttaaga gaattcctaa aatcaagtga agtatcatca cttggtaaaa	540
tttcataacc gttggttctt atttctatgt gtgccttggt ttgcaggaga taatattca	600
tttccaacca atgatattcg tacacatagt caaacaaatg tttgttttg ttattatatt	660
gagaaaagaaa caagaaagag agagagagat agataagacg aaggaagtga agcttccaag	720
cggccaccgt taaaatctc gtgtgcaagt ttcaaataca agtggccggt ggtctccata	780
atttgatcgat catccaatta aaaaggaaga aaaagcgtgt ttatatacaag aaaactcatt	840
aaaatagcaa gtctagaaat atctcaacac taatctacca cgtctattac acacacacac	900
acacacacctt gatctaattt tattttcaag attcaagaaa atacccatcc cattaccaca	960
acttgaccac acgcctataat ataaaacata aaagcccttt cccc	1004

<210> SEQ_ID NO 41

<211> LENGTH: 1000

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0102

<400> SEQUENCE: 41

atttgggtga taacgtttc actcgactaa ttatatactt cagaaggata gtaatagaat	60
acccaaaataa ttaaatgatt ggttagtgcc tttagtggaga ctttttaacc gattctaata	120
gactaatgtat gtagctaagc atttattttgg gatcatcaact gtttggaaac gtgaaatgtg	180
ataaaaagtttta tgaaaacgatt aaaatataaa ataaccgtac aaaacattat gtaccgttt	240
tttctctgtt cttttggcga tttggtttag ttcgttacac tctaaatgtt attgcagata	300
tatataataat gatgcatttg catctgagga acatataatt ccggtaaca cttccaaatc	360
ttatatccgtt ctaggttaggg attttataaa tcattttgtt catcatcgat tatgtttgtc	420
ggctttgacc ataacgcaga gatataagaac tagctttac ttaacttttta gattttat	480
ttgatctaga gttaaatggaa gatataatgt gttttgtta gatttttgtt ggatgtgaga	540
gtttgtttttt agtttcaagt tgagaatata aggcaagagg agactctgag gcaatcagag	600
gttttgattt gcaaaatatac caaaaggccc aaaccaagtc gaagccccatc tcgtacaaaa	660
aaagaaaagag atctgtttaaaa aaaaatattt tttgatattt ttacaaaaat aagtgtaaaa	720
cttttattttt tcaaaaatctt caatctttaa aaactctcat cactcctacg aaagcgctgt	780
agagttatgtt gacattccctt aatagcatta ctcacaagtc acaagttcaa aacgtctgac	840
tgaaacagaa acaaggccctt gttgaagtct tgaagaagag acatttagtac tcgtcgatata	900
gccatataaaag gtaatataacg aaattttctt gctaattctt tcacccctt ctacgcgttt	960
cactttcaact ttataaatcc aaatctccct tcgaaaacat	1000

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<210> SEQ ID NO 42
<211> LENGTH: 1004
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0103

<400> SEQUENCE: 42

gttttgaaga acaaatctgga tcgaaatcta acataaggtc atcgtattca agttacgcag	60
tcaaggactt gacatcatcc tactctggtc tgaggttacc acttccaaag atgggatttt	120
tcgactcggt atgcttccta agaaaattcgt tttattgaac ctagcaaata tcttgtaatg	180
taagattcct gagatgtatga agaaaaaaaca aacttttgtt acagcaggag aacggagaga	240
aagaaaaaacag agaaccaaat gcttcttgaag caaacagaag aagaagacac aaatccaaac	300
ttgagacttc ttctacacca gaaaaccgca gcattctggg acaacgcaaa acacgaaagt	360
gaaacacggca atgatataata tgcgttgggt gcgttacaag gcatcggtt caactgttga	420
gttggataag tcaactgtct tcttttcctt tggttgttagt agctgccttt tttttccctt	480
gttgctttaa gaaatagccc gaaaaaaaaaaga atgttctaca ttccggagca gaaaactaac	540
cgaatgagtt ttggcggca tcatcggtc gatcagatata atttttagttt acgaactgtt	600
ataaaaaaaag ccataatttt gtgtttagtt tgcaaaatac cttataactt gttatttgag	660
attgcaccc tcataatattt aattcgtaag agtattttt aagtaagctt tagtataat	720
cctttttcc tttaaagtaa gttatgttc tactaaataa tagtaaagtt gaagaaccgc	780
tccgtttta caccatgcac gtgttatcta acaaagaaaa tatggcacac ctaatggcta	840
atgcaaagga caacacaatg aaactaactt gactctgtgt tatagaaacc catagacatc	900
tgcatacatc ctatgtttt gataaattgg actcaaattt ctgaggacaa tcatacgaaa	960
caatcacatc atcgcaatat acataaacaa aagaggaaga aaaa	1004

<210> SEQ ID NO 43
<211> LENGTH: 1003
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0107

<400> SEQUENCE: 43

taacaatcct tggaaacatt gcattccatag atatccgggtt aagatcgatc tttgaactca	60
taaaaaactag tagattggttt gggtggtttc catgtaccag aaggcttacc ctattagttt	120
aaagttgaaa ctttggcccc tactcaattt ctagttgtgt aaatgtatgtt atatgtatg	180
tgtataaaac gtagtactta aatgactagg agtgggttctt gagaccgtt agagatggga	240
gcagaactaa agatgtgac ataattaaga acgaatttga aaggcttcca ggtttgaatc	300
ctattcgaga atgtttttgtt caaagatagtt gggatttt aaccaaaagaa aacatttttt	360
aaatcgtat ccggttacgt tcatgcaat agaaaatgtt ctaggtatctt attgtatatt	420
tagacttaaa gagtctcttta agattcaatc ctggctgtgtt acaaaaactac aaataatcta	480
tttagacta tttggccctt aactaaactt ccactccattt atttacttgag gtttagagaat	540
agacttgcga ataaacacat tccccggaa atactcatga tccctataattt agtccggagg	600
tatgccaatc agatctaaga acacacattt cctcaaattt taatgcacat gtaatcatag	660
tttagcacaatc ttcaaaaata atgtatgtt aaagacagaa aatgttagac ttttttttgg	720

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cgttaaaaga agactaagtt tatacgtaca ttttattttt agtggaaaac cgaaatttc	780
catcgaaata tatgaatttt gtatataatat ttctgcaatg tactattttgc ctatTTTGC	840
aactttcagt ggactactac tttattacaa tgtgtatgga tgcatgagtt tgagtataca	900
catgtctaaa tgcgtcttt gtaaaacgta acggaccaca aaagaggatc catacaaata	960
catctcatag cttccctccat tatttccga cacaaacaga gca	1003

<210> SEQ ID NO 44	
<211> LENGTH: 1024	
<212> TYPE: DNA	
<213> ORGANISM: Arabidopsis thaliana	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<223> OTHER INFORMATION: Ceres Promoter YP0110	
<400> SEQUENCE: 44	
gggatgcggt tccgttctt cttgtatctt gacgagtcgg aggacattgt tggatcccag	60
tgcataatggta atataaaaaca agaaaacaag agatTTATAA ggacaatcac taaatgcacat	120
ttaatttgatt aaacattttt tcattaataa ttgttatgtt ctaacttcaa catttaataa	180
ttttgtttaa gatacgttta catcagagac tattaatatt ttacaggtt gtaactttaa	240
actttgtctt gaatcgaaca tgactataga ttttgggcaa acttaaagat aacaacattt	300
ccgtttttttt tcaaattattt acaaatttcaa ctgatattttt agacacaaca cgattacacg	360
taataaaaaa agaaaaagat aaaaagat aagaaggat cgattctgtt tggctctgtt	420
tagtgagatt caaagttaag ctttcccttt caagacatgc cttcttaaac cgggaatgtg	480
aacgtttcta atgttagtccg tccagttaat gcttccaaca tcaaatttcaa attctcttt	540
ctcgttcttctt gacatattttt ccattttttt ctggggattt gctgttatca aatctgtttt	600
agaaacccaaa aaaaaaaagat gaaaactttt cgggttaccgg ttttgcgttgc tcttggaaatt	660
agaatgtttaa tgagttctgtt cttttttttt accatagaaa gtgtatggct cataaatagt	720
agcaagggtgt ttggcttgc caacagattt cttgtatataa aacttttagct tctgtatcat	780
cttactatcc actgaactca taccactcat caacccactc cgttcttgag catctcttca	840
caaattgtatcc gagaatcat caacggattt gaaaagttt atcaaaccgc ccataatagg	900
atcacctttaa gatgtccatgc atggagatgt ttgtatgtt ttataaaagaa gctccgcataa	960
gtcttcgaaa accagcgggt ttatcgccga agaagcgatc tgatacacgt ttatttcagg	1020
ttcc	1024

<210> SEQ ID NO 45	
<211> LENGTH: 1024	
<212> TYPE: DNA	
<213> ORGANISM: Arabidopsis thaliana	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<223> OTHER INFORMATION: Ceres Promoter YP0111	
<400> SEQUENCE: 45	
cgttggatt tagtctatac attataggcc gcaagtttgtt ggatTTAAGA attatataaa	60
aacttgaaat atatagtttt tatgcattttt cctttttgtt aatacataaa ccaaataatga	120
gatagggttaa tctgtattttcc agataatattt aaattccaaa caatattttt acttggatata	180
agaaggcaat taatatctt cttgtttatgg caagttgtac caagttgtat taaactttaa	240
atgcaatgga agagttttttt tggaaattttt aatcctttat cacacattca aacagatctc	300

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ctgaaatctt ctcttccaaa cttgtacttc tctgatccaa atgtaggctc caaaatata	360
acatttacca ttactaagt ccacaactcc tttcttgct ccttcaaaaa tgactctgt	420
gtaaccacca tatgactccg acagttcgcc attgccatga tgagagctt aaaattcacc	480
ttcctgagca tttcaagtct tcactccctt agtttgacctt gaaccaagat aaaatgcctt	540
tgtcgcccg taatatccat cctgctttgg acggcatcat agttacatc gatccatcct	600
atttacaatg ttattttagt attaaaaaca tgacaataaa ttttgttta aacatattca	660
aatacaaatat gattggattt ataagtaatt gtaatatgaa atgtccttag taatatgtt	720
aaaaatacat agatacacac acgtactaaa agaggcaacg cgggagatgt cattagagga	780
agaactagga agcagagcgt tcatgcaaaa tgctaccaaa aacgttaatg caatatctca	840
actaatcagc acagttccatt tcactactgag aatgtaaaaa ccaatcagca tcgtccattt	900
tttcatctaa ttatgttta actcttaattt ggccacaactt cccaaccaca tgacgcttt	960
tctatccctt ttatataattc ccatctcaaa tgttcttgg gacacaaaat atcataaaca	1020
tata	1024

<210> SEQ ID NO 46
<211> LENGTH: 996
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0115

<400> SEQUENCE: 46

gtcgatttggaa ttagtgcacat tctacatata taatttattt gtttaaggcac tttagacagca	60
taaattcttt ctaattatataa aaatctaacc ttgttacattt gtacatctat aaattacttg	120
aagaaaataac gagttctattt tctttttaaa aataaaaat actataccat atctcagtgaa	180
ttaagttgaa ccaaaaaggta cggaggagaa acaagcattt gattcttctt tattttttt	240
tattcatctc tcactaatgaa ttggggagaa aaaaagaaaa tacctaacaa acaaataatata	300
attgtcatac aaaaatattttt ctatattttt agttaatttag tttatattcc tcactttca	360
gggcttatata aagaaagtga gcaaacacaa atcaaaatgc agcagcaaat actatcatca	420
cccatctcct tagttctattt ttataattcc tttttttttt gttcatagct ttgtatatt	480
agtcttattttt ctctttaagg ctcaataaga ggaggtacta ttactacact tctctctact	540
tttacttgta tttaggattt aatccgtttt aaattcaaaa ataaaacttag	600
agatgtttaa tctcgattcg gtttttcggc tttaggagaa taattatatg aaatttagtat	660
ggatatctttt actagttcc attcaaatgaa ttctgatttc aatctaatac tctcactttt	720
taattaaactt atatgtatgtt taatttcaca ctgttaattt tctaccatgtt catgtatatt	780
agagttgcattt agaaaaattgtt aaaaacatcca tttgaattcg aatgaaacaa aatgttttaa	840
aataaaaattttt tggtttttaa aagaaaaatcc taaaactgaa ttatatcggtt taaccaagtt	900
gtaaaagtca taaaacgttag tatcttgtaa atcgctttc cacggccaa atagacttct	960
agtaataaac aagtaaaactt aattttggttt tcttac	996

<210> SEQ ID NO 47
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0117

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<400> SEQUENCE: 47

gtcagtgagt	cgattggatc	acagtcctt	atgataaaac	aaactcataa	ttattccacc	60
gacaacatgc	gttttaaatt	attttttctt	aaatttatatt	atattatatt	gatatcaacc	120
tagctaaaat	aattcggatg	gcgaaatcg	acaatttta	atagaaaaaa	tgggtatgaa	180
gatagtctat	gattccgttc	ttagcgacta	gagggacctg	ctcaaattctc	ccgggtgata	240
cgcgatgtca	agctcaatag	aaccccacaa	ccgacgagac	cgagaaatcc	ttgatttggg	300
ctagaagatt	ttgaaataaa	ttaatataat	tctaagtaac	ttgcttaaat	ttttttcaa	360
actctaaaga	cataactaac	ataaaagtaaa	aaaaaaaaag	ttaatacatg	ggaagaaaaa	420
aattaaacta	atgatttagct	ctctaacgtg	ttaatctcg	tatcaagttt	ttttttaaaa	480
attatattgc	tattaaaca	ttgtactatt	gtttcttattt	tgtttagcta	ttattcttgt	540
gaaatgaaaa	gttgtgttta	ttcaattact	aatggcaat	atttatctg	gaaaactata	600
cctctaattg	gattaggccc	tagacatct	ctttagctta	ttgacgttaa	aattatccc	660
aaaactatta	aagtttagta	gtttgaaaga	tgcataaga	cctactcaga	tagttaaaag	720
tagaaaaacta	cagtttagtgc	gattatattt	taaaatataat	aaaacaatct	tattaaacta	780
aatattcaag	atataactc	aaatggaaaga	taaaaacatt	tagtctgtt	ccactaccag	840
ccttagctgt	cactaatagt	cactttggaa	ctgagtagat	atttgcacatc	tgagttacca	900
tggactcaaa	agtccaaaaa	gagaccccg	gtgaaaatgc	taccaactta	ataacaaga	960
agcatttaca	gcggtaaaaa	agtatctata	aatgtttaca	caacagtagt	cataagcacc	1020
attg						1024

<210> SEQ ID NO 48

<211> LENGTH: 1000

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0119

<400> SEQUENCE: 48

tacccaaaat	aaggagttc	caaaagatgg	ttctgatgag	aaacagagcc	cattcccttc	60
cttttccccct	tcccatgaaa	gaaatcggt	ggtcctcctt	caatgtcctc	cacctactct	120
tctcttcttt	cttttttct	ttcttattat	taaccattta	attaatttcc	cattcaattt	180
cagtttctag	ttctgtaaaa	agaaaataca	catctcactt	atagatatcc	atatctat	240
atatgcatgt	atagagaata	aaaaagtgtg	agtttctagg	tatgttgagt	atgtgctgtt	300
tggacaatttgc	ttagatgatc	tgtccat	tttctttttt	cttctgtgt	taaatatatt	360
tgagcacaaa	aaaaactaa	taaccttctg	tttcagcaa	gtagggtctt	ataacctca	420
aagaaatatt	cattcaatttgc	aaaacccata	aacccaaata	gatattacaa	aagggaaagag	480
agatattttc	aagaacaaca	taattagaaa	agcagaagca	gcagtttaagt	ggtaactgaga	540
taaatgatat	attttcttctt	caagaacagt	ttctcattac	ccaccttctc	cttttgcgt	600
atctatcgta	atcttgagaa	ctcaggtaag	gttgtgaata	ttatgcacca	ttcattaaacc	660
ctaaaaataa	gagatttaaa	ataaaatgttt	cttcttctc	tgattcttgt	gttaccaatt	720
catgggtttg	atatgtttct	tggttattgc	ttatcaacaa	agagatttga	tcattataaa	780
gttagattaat	aactcttaaa	cacacaaagt	ttcttttattt	tttagttaca	tccctaattc	840
tagaccagaa	catggatttg	atctatttct	tggttatgt	ttcttgatca	ggaaaaggga	900

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tttgatcatc aagattagcc ttctctctct ctctcttagat atctttcttg aattttagaaa	960
tctttatcta atttttgtt gatgtcatat ataggatcaa	1000

<210> SEQ ID NO 49
<211> LENGTH: 999
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0120

<400> SEQUENCE: 49

tagttttga tttaatctac gttttctta atcataaatg ggtaattatt agttttgca	60
aaatcaaaat caaaaattt ttctaaacac tgcaaccatt taaggcctat atcactcaga	120
aaatttctgg tgggagaact aatcgttgt ctttctaaa tctcacatat tagaatttag	180
aatttagtgct acataataa atattagttc agctcggAAC aactatTTT tggtaaaaca	240
gagaacttaa acaaatgcattt ttttatca acatgcattt tgaattgaat ataaaatttc	300
ataattgtaa agacataaaat tacataaaaat tttacatgaa aaaatagata tagaaagaaaa	360
atgaaactaa ctgatgatat gctctctaaa tttttaatc tcataacaag aattcaattt	420
aatttagtca tatttttgtt taatataaca tttacctgtc taagttggaa ctttcatttt	480
tttctgtttt gtttagtcag tattcttaat gtgaaacgga aagttgaatt tattcaact	540
taaattcaat agcattaatt aaaggcgaaa gctattatctt ctacatgtgg ttcaaactag	600
acatccaattt taattagctt attgacgttg aaatgttttcc caaaactact atatgttgc	660
aatttggaaag atgcatcaga actactcaga caggtaaaag tagaacctct agctgtgtga	720
attgtatgtt agtccataaa gaacatcttg taaaacttcat acttaagata tatattacaa	780
tatatacttg aatggtagat aaaaacgatt agtctgatttctt ctagcataact cacaactatt	840
tggaaatgag taagatatttgcattctaga gttactacta tggagacaaa agtcaataa	900
aagagacctc acgtgaaaat gttacgagct agtaaaaaaa gcatttacac taacggtaaa	960
aaaagtatct ataaatgtttt acacaaggta gtagtcatt	999

<210> SEQ ID NO 50
<211> LENGTH: 999
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0121

<400> SEQUENCE: 50

ttggattttt ttttttgtga gtcagcagac catctaatctt ctcttttcc accacagcct	60
gttttctatg aagcattttgg gcttacgggtt gtggaatcaa tgacttgc actcccaacg	120
tttgcattttt gtcattgggtt accccgcagag attatcgaaa acggagtttc tgggttccac	180
attgacccat atcatccaga ccaggttgca gctaccttgg ttagcttctt tgagacctgt	240
aacaccaatc caaatcatttgg ggttaaaatc tctgaaggag ggctcaagcg aatctatgaa	300
aggttggccc attctccatttgc acaggcttaa caatacaact tgatcgctt caacaagatg	360
atggcttaat aaggatttttgcattgtatag gtacacatgg aagaagtact cagagagact	420
gcttaccctgtt gctggagtttgcattgtt gaaacatgtt tctaaagctcg aaaggagaga	480
aacacgacgt tacctagaga tggtttactc attgaaattt cgtgattttgg ttatgttaac	540

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ccactgttat tctttttagat tctacatcta ctttacttac attattcttt tcttcgggtt	600
gcaggccaat tcaatcccgcc tggcaacaga tgagaactga tcatgacagg gtaggatTTT	660
atttcctgca ctttctttag atctttttagat tggatTTT tgaataaaaa ttgttgggtt	720
ttgtttcctt cagtgggttT atttggact tattttgtgtt aatgttggTT tggctgtct	780
cTTaatatca ataacaataa aatttactgg ttggatCTCA agatctaaca atagttacta	840
tttttagagg taaagacacc aaccttggta tattttgtcg agagctaaaa ccttgacttG	900
ttggggaaaac aaaactctaa tgacagaaaa tctgacatga tgccttataa ttcacagcct	960
catgttctac ataaatccta acaatagcac tttgtttct	999

<210> SEQ ID NO 51

<211> LENGTH: 1004

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0128

<400> SEQUENCE: 51

gataaaactga taatggaaaa gaacaaagaa accagtttt aactatttgc atatgttaatt	60
tattttgtgc aaatttatatt tagttaaaat gtttcctcta tttatataata tatatatcag	120
tcaagcacta tgtataagaa atgtcaattt ataaatTTT acatgtccTT taacagaaaa	180
aaaatgaatt tttacatgtc attcatagag agtcactcgT ttatttctta tatagagaat	240
aacacactca catgcataatg catgcaatata gatacattt atgacaaaaa taatcaacgg	300
aaacggtcaa gacataattt gataaacaac ttgcacgatg cacagatctg atcaaataata	360
taactcttta acatatccaa aatattcaaa aagaaaaact cgatccaaac tagcaacatc	420
acgctcacgc ggtaggctaa aaatttatta atctccaaaa gtcttctta tgaacactgc	480
aaacacaaca acttggaaaag tcatataggt ttagatgtg acgcgtatTT gctatcgctt	540
accggagttgg ctcataata caataaacaat tacgtaaaag tcaaagtcaa atatatttag	600
tcaactataa ccattaatcg ggcaaaacct ttagctgtca aaacaacgtg aaaacgatata	660
ttgttatataat catcaagaat cagtagataa gagaatgatt taatcccctg actattacaa	720
ttttgggtgtat ataaacagtc tctattggTT tttattttttt gttttatTT ctcatgacct	780
atagagagaa ttaggttagtt tcgaaaattt gctaataac ttttggaaaact tactgtctac	840
tttgcttaaa ttctctacac tttagttcggtt ataaagataat tgcggacta atagttatc	900
ccttgacaat ctttgatatt ataaaaggTT tagttatct cttctctata taaatattca	960
tacaccagct ttcaaaaata tataatccaa acaccaaaaaa caaa	1004

<210> SEQ ID NO 52

<211> LENGTH: 1001

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0137

<400> SEQUENCE: 52

gtggcacatg ctgaaaacccc gagcatctct ccggaaagaca cgcgtcgTT gctccaaaga	60
aaacagtcac agctgccccgaa gaatctccgc cgtcttcttgc tgccacccggaa aaaactctct	120
ccaccacTTT cagtccccac ctcgtgttat atccactgtat tcctcgtagc accatatacg	180
cctaataaaaa ttttatgtat caaatTTTaa gacatagccg aaactacact atactagaca	240

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ataataat atattgttcc ctgaaaaatt atggttcat gagaaacatt aatcatctat      300
aaaacaatt agctatggca tcgaagagtt atcaatcaa actgatgaat ctttacttaa      360
tatatacaac atatcttac cttgcggcg agaagatcg cgagagaagc accccagcca      420
ccgtcaactaa aggattcttc agtcatggaa tcaccaaaga gaaaaaccctt ccgtctcatc      480
atcttccaca caatcttctt gagaaaatct gagagataag aaaggtag tggtttgct      540
gaagtatcg tgtttattt agtaaagaaa tgctttattt attgttgggg gaaacataaa      600
taaataaaagt aaaagtggat gcactaaatg cttcacccaa ctaatcacccg acctttcatg      660
gtttatttgcg aaatacactc atagatagac atacaatacc ttatgtacgt aaataacatt      720
ttatgtcg acacttatgt aagtaacgc tagatttattt tctatgtgat tgccactctc      780
agactctcg tttcaaccaa taataacaat aactacaaca acattaatca taaacatcg      840
ctctggttta caattaaagc tttagattaag aaactgtaac aacgttacag aaaaaaaatg      900
ttattnacgt ttgttaagat tagtctctag aatcatcacc gtttttata tattaatgat      960
tctttttat atataaaacc tttctcgaaa tacccatgaa a                                1001

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<210> SEQ ID NO 53
<211> LENGTH: 1001
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0143

<400> SEQUENCE: 53

atacaacaga tggcagatata cgagttaaat acgtgaatca gccgttacga tattttaaaa      60
ctagaaaatt attaaaaat attgcaaat accatthaat ttcattgttc ataaaaaaaaa      120
gaaattcaaa aactaaaaaa ctgattcaaa aatttggatt aattctcatt aacagtctc      180
aacactacaa caacatgtt ctaattttt ttatattta ataattaaac aatataacg      240
tctgcacatt gttgctccga cataatctag tataaaaata gttcagcat atgtgaaaag      300
caagcagcat ttatcactca atactttaa ttttatctgt tttatgtt aaggttttgt      360
agcttaaga aaacgcttat aatataaaat aacttctaaa agatatttca tgcgtataca      420
ataaatattt gtgaaaaaac atttcgaaaa cgtgtacaat atataaacta ttgtgttatac      480
tttgacatt caaacaatg ttgacaatgt aattttatcc atgatatgat tggccaatta      540
gttcgcggat aaaaatccgt atacgagtaa aagtaagata aatttcgca agaagattt      600
tagcaggaaa tctaagacaa gtgtcatgaa cgtgtcaatc aacaaacgaa aaggagaatt      660
atagaatcca gattcgacgt accacattaa taaaatcaa aacattttat gttatTTTAT      720
ttttgtctg gcagttacac tcttttcat tgcgttccata aaaaaatcac tcgcgttgcac      780
gcataatatac acaccatagt aaactccgca ttttcttcat ttatTTTAT tgcgttaca      840
ctgacacaat ctttactat tttctttgt ttttcttcat ttatTTTAT tgcgttaca      900
aaggtaacaa ataatcttt taatgttactt ttatTTTAT taaatcttag attgtatata      960
gaatgcatgt taatatttca agatTTTAT gtctaccaaa c                                1001

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<210> SEQ ID NO 54
<211> LENGTH: 1003
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<223> OTHER INFORMATION: Ceres Promoter YP0144

<400> SEQUENCE: 54

aaacgttgca agattattga ttgtgagaaa gagtgctcaa ggttagtactg atttctgtaa	60
agctcacggt ggtggaaac gatgttcttg gggagatggg aaatgtgaga aaatttgcata	120
gaggaaagaa gcggtttatg cgctgcgcat aacactatta tgcgtcgga gaacaaagat	180
ggaagcaaga gcggtttgat tggaccggga ctcttagtgc gcctgtttt tggctctact	240
tctgatcatt ctcagtcgtt agctagcgt gtctctgatt gtactgatc tggttgcacga	300
atacagtttga aataaggca gaagaacaag aagatgtatc taccgtatc ggttcttagta	360
ccttcataaa tgaatctcc aagtaattca catgaaggag aaacaaacat ctatgacttc	420
atgggtccgg aggagagagt tcacggcgtt gggcttagtaa tgcgtttact tggtggctcc	480
attgatcgaa actgaaagcc atttatggta aaagtgtcac attctcagca aaaacctgtg	540
taaagctgtt aatgtgtgg gaatctccga atctgtttt agccggttac gttatgttgc	600
atcaaaaaactt caagatttgc tggatattgt tatgctggat cgggtggtaa accacttccc	660
gggttgcataa taaataaacgc tttttgtttt ataatctttt tcactaaacgc gcagtatggg	720
ccttttagtgg gcttccttta agcgaccaat acaatcgtcg cacccggaaatc tactaccatt	780
tataggttta ttcatgtaaa acctcgaaa atttgagagc cacaacggc aagagacaaa	840
aacaacttgc agataaaggaa ataaggaagg cttcctacat gatggacaac attttttcc	900
acacaaatttc tcataataaa aatcttataaa tacaaataact tacgtatcaa tcattcaatc	960
tagtccccat gtttaaggt cctgtttttt gtctgataca aat	1003

<210> SEQ_ID NO 55

<211> LENGTH: 1004

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0156

<400> SEQUENCE: 55

ttggtttgca ttgtgaagat ttgttataac tatagaacat tgaattgtatgt gtgtttaagtt	60
cttacacaag cgtgtttctc gggttgaact gtttcttttgc tatgttgaat cagagcttag	120
ttttaggaa ccagagtatc tacttagtca ttctctgtatc ctaagtgcata aggttctacc	180
tagttgcctt ctagggccctt atgttattgtatc taacttgcata agctatttgcata acacttgcatt	240
cttagggagac ctaagttggat acagccagat agagtgtatc ttcttgcata ctagtgcata	300
ggatcaagctt gccacacata gttcaagggtt atgctctgtatc tgggtttgcata cagattggagg	360
acaaatcttat acaaggaaatc agagtctttgcata atgttgcata aagaagaaga	420
aggagagatc ataaagaaatc agaaaaggaa aacagaaaca cgtgggagaa catccaaatc	480
aggaagcaca cgcggatctt catgcaaagc tccccggatcc tcccatgttgc tcccttctc	540
cctttgtccc cctccctttt ctttttttgc cattttactc ctttttttgc cattataaca	600
cgaatctttt ttatcataat tttttggatc tgggttttttgc tocaataaca ctttttttgc	660
tacttccat tctcactttt tcatataaga aactcactttt gggaaacttgc tgggtttttgc	720
tgacaaggatc tttagagaa agtgtatgtatc caaatctaaat gttttttttgc aataacccatc	780
cacaatgtttt ttgatccatc gtaagattcg aatatttaggtt tattttttttgc tagggataaa	840
acttacttttcc aaaagcggttca ataaggtaat actttccatc atgtatcataa gtacggacac	900

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tatgtttttt tgtttgtttg tgtttattct aaaagaaaagt agcttttaat tgaaatgtcc 960
tcggaggcac agtttaaagt tcgactgtaa cagtttctaa ggca 1004

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<210> SEQ ID NO 56
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0158
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<400> SEQUENCE: 56

tttagatt aatagattgc attgeattgc ttgtgc ttttacaaa ttgtctccca
actccatcg aacatctctt tttgtgtata taagattcag acttgttata ttttttttat
aaatatgtta ttagcatctt aagttaaatt gatttttat atctgcatta aggattacac
gactatattt gcgattgtgt gttggtaaa atataatttta ggattgtctt taactacatt
taggattata tgactatattt tggttaaata taaaatctag ctgtgattat tagtattcaa
aaataagtat cctaaccat taaaacaacg gctattgggg caaattagaa cattttagtg
tgtccaaat ataatggtca tttagtcata ttccctcttag ctcatcgca gcataattga
atgattgcct tatTTTGAAG agctttcca cttcccaa atcttaggtgg gatTTTTG
tttgacctt cattttctt gtttaccatt tttagctaa ttatTTACGA ttacaaaaga
tatcaaaagt tggatcataa tacaattttt agacttactg tagaaaattc gtatgtacaa
gtacaacaaa ttcttcataa taaattttga aaattctatt acaaatgttg taagaaatag
aatttgaat atatataaac taaggagaaa aaaaaagaga acatgcattt ctctagtcag
agtgacccaa catcaacgag ataagataac ataaaaacca actcaccata actaaaaaca
tcccaagaga tccaaacgatt catacaaac acaaaaacat cgaacgatca gattttaaacc
atctctggta tctccaaac acaaaacatt ttttttttctt ttgtctgaa tggaaaaaaa
gcatgcgaca tctctgtgtc ttatcttctt ctccctttt ctggaaaaac tgaaccttta
atttttctt cacaatctctt ttagtttctt qaaadctqctaa

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<210> SEQ ID NO 57
<211> LENGTH: 1005
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0188
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<400> SEQUENCE: 57

gattggatg aaatttcgga gaccaacaaa aaaaacttta ttgagcttg agtgaagcta 60
tatatatggg gcaagatcat aatatgttta tatkccctt ttcgttaact gaaaataata 120
gttttgagaa atatatcaaa tggttaacag acatcatctt tgaaaaataac catcaatgaa 180
gttaatattt ttattggcat atggtttacc catcttaatt ttaatgcac caaacaaca 240
agaaacaaaaa actgtataag atacaagggtg ttttacgatt ttccgtctta aaaccgaaat 300
atttttgttc ctacgacttt aaacggactt tgcttaagt gtgtgcgtgt aagctcgatc 360
tccctcgatt gtcataaca ttcaccaata tcagccctta tcacacgagt gaagggttgt 420
atccggctta atgaaaacag agaaaatattt caatatgatt cctattaaat tttaaatctt 480
ttttctcaat ctcttagattt tcattaaaag catcatgatt tttttccact atgttcataat 540
atctctatca cagttttagg tacattgttag aaattggata agatacgtca tacgtctaac 600

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atgaatttgg tctagcaagg aagggttgag ataataagtg aaaagaaaaac acaagataat	660
aaattataat ttataaatgc tttatagtat tgaaaaataa gatgattttt tttttttta	720
ataccggatt ggctgatcca cttatgatga ctcaaatgtt attaagttc aagacaattt	780
atgatgacac aaatcacaat gagtcaatag tagccacgaa gccagaaaaaaa aaaaatgtac	840
tacaaaaaga taatgatagt acaaaatgtat acgtcgact gcccacatgta cgacacaact	900
cgattaccaa aaagcagagc catccaaacca taaaactcaa aacacacaga ttccactggc	960
gtgtgtctc ctcacttcac tcgtccttga aacttgagg actga	1005

<210> SEQ ID NO 58

<211> LENGTH: 1002

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0190

<400> SEQUENCE: 58

taaatagtga cattggtaag aaaaaaaaaa acactattaa atagtggaaaa aatggtttat	60
aactctctta attaacatta cttattattt ctgcaccta aaatctccca caaaatattt	120
gttgtaaaac acaaattttac aaaatgattt tgtttttaaa ttagtaacac atgttcatat	180
atacgttaat aagaacatac cctatatgtat ttatataaaa aaaattctt tgagacgtct	240
tattctttt tcttaataa tatgcaattt tgagagttt gatttgaatg gtgcatttt	300
aagcaaactt gaaccaaaca tatttcatga agtcaaactt gaaccaatgtt gatcataat	360
cacagtgttc gcagtgttaag gcatcagaaa atagaagaag ggacatagct atgaatcata	420
taatcttgac acatgtttt taggttttag gtgtgtatgc taacaaaaaa tgagacagct	480
ttcttctaat agacttaata tttgggctaa atgtaccaca gttgtgaatt tcttacaaaa	540
atggggccgag ctacaaaaaa ctacaggccc actctcaact cttatcaaac gacagcggtt	600
tacttttttta aaagcacaca cttttgtttt ggtgtcggtt acggtgagg ttgcgtcgctc	660
ttccctttaaa ttgaagcaac gggtttgtatc cgatcaaattt caacgggtctt gattacacaa	720
agccccggac gaaaaacgttg actattaatg taggttttaa ttcagccgt taatctacaa	780
atcaacgggtt ccctgtaaaaa cgaatcttcc ttcccttcttcc acttccgggtt cttctctctc	840
aatcacctca aaaaaatcga tttcatcaaa atattcaccc gcccgaattt gactctccga	900
tcatcgtctc cgaatctaga tcgacggat caaaacccttta gaaatctaaa tcggaatgag	960
aaattgattt tgatacgaat tagggatctg tgtgttgagg ac	1002

<210> SEQ ID NO 59

<211> LENGTH: 995

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0212

<400> SEQUENCE: 59

agtcgattgg tacactctta atttaattttt agtaagagat caacaaaaat atagaatttt	60
ctttatcg aagtgttacg accttatata tatagaaaaaa aagcatagg tgaatctcta	120
aattgagatt gtgtgttagt aaacatattttt agtttttagt ttttttaaga aatgaatctt	180
tttgttggatt aattcaaaactt agtagtcatt aagattccgg agattccaaat ttagaaaaagt	240

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caaagattca aagaacaagt ccaggtccac atgttgaatc cgattcatca tccactcatc	300
cttcataatct tcctccaccg tctccgccc aaaaatcaat aacaataaaa aatcctaaaa	360
aaacatattt gatttgaaa aaactttatc atatattata ttaattaaat agttatccga	420
tgactcatcc tatggtcagg gccttgctgt ctctgaegtc cttattatc attatttta	480
aatttgctc tctcagaaaa ttacgcccaca atcttcctct ttccctttc cgaaaacagc	540
taatatttgt ggacctaaac taaataacgt agcctctaga ttttatataa ttactaatac	600
tatatgtac tactgttat tatttactcc aatcatatat gataccaatc aagaatcact	660
acataaggtag aaaacttgc aatgagtcca ttaattaaaa ttaagaataa actttaaaatt	720
ttatggtatt ttaagattcc ctttgattt gtaatgacaag aaatcagcaa attagtcgt	780
actcgtaaga ataaacaaga tcaatttttta ctttctttac aaagattccg ttgtatattt	840
agaaattttt ttttgtact gttttttat agattaattt atctgcatca atccgatcaa	900
gaagtgtaca catggcattc tatatatatc taacaggtaa aacgtgtatg tacatgcata	960
aggttttacg tgcttctata aatatatgtg gcagt	995

<210> SEQ ID NO 60

<211> LENGTH: 1024

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0214

<400> SEQUENCE: 60

ccagtegatt ggcgectcgc atgcctatca tatttaaccg tcaataatgg atttggcggt	60
tttggtaggc cgggtcaacc ggattaaaag aaaacggttt ggagtccctc cttgcatttgc	120
aattttcaca cattegggtt ttgtgatttgc tctgtcataa tggggccggc acatatggtt	180
cataaccat gtgggcctat ggtataattt ttccaaattt aactattgtt aggtcgatcaa	240
aacaaaaaac aataaaaacg agtggaaatac acataccaaa aagaatgtga tgaacatitag	300
taattttatt ttgtatggta atgaaaaaca aaataaatgc atcttggcat cttccgttgg	360
aaagcgcaaa tagggcagat tttcagacag atatcactat gatggggggt gagagaaaga	420
aaacgaggcg tacctaattgt aacactactt aattagtctg tagttatagg actttttttt	480
tgtttgggcc tagttatagg atcataaggt aaaaatgaag aatgaatattt agattagtag	540
gagctaattgtt tggagttaaatgatgacgtt taagaactgg gaagtggaaac ctcctgtatg	600
gtgaagaaac tatacaacaa agccctttgt tgggttatac gtattaattt ttattctttt	660
atcacaagcg atacgtatct taagacataa taaatataata tcttactcat aataaatatc	720
ttaagatata tatacgtat acacctgtat atatataata aataggcata tagtagaaat	780
taatatgagt tgttgtgtt gcaaatatata aatcaatca aagattttaa aaccacccat	840
tcaatcttgg taagtaacga aaaaaaaggg aagcaagaag aaccacagaa aagggggctaa	900
acaactagac acgttagatct tcatctgccc gtccatctaa cctaccacac tctcatcttc	960
ttttcccggt gtcagttgt tatataagct ctcactctcc ggtatatttc cccattgcac	1020
tgga	1024

<210> SEQ ID NO 61

<211> LENGTH: 911

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

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<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0263

<400> SEQUENCE: 61

atcttagctgt ggattccacc	aaaattctgg cagggccatg	atctaaaaac tgagactgcg	60
cgtgttggtt tgcagtgatt	tgtatttcat atttgcacca	tcctacacag tccacttggt	120
atcgtaacca aacataagga	gaacctaatt acattattgt	tttaattcg tcaaactgg	180
ttttacctt tagttacata	gttggattttt catttgggg	atgtttatg gagcacaata	240
atgtgcaaca aagaaagatc	atagtggatt aatatgtga	gaggcagaa attttgggt	300
aacaaaaaaaaa agttacaagg	actgagattt tgggtgggg	aaagccatag cttttaaac	360
atgattgaac taaaagtga	tgttatgggt tgagggaaa	aagggttgc tcaactaaga	420
tagttgaagt aatgtcttaa	actaaagtaa accaccgggt	caaccgtggt ccggaagcat	480
ctctggtatg atttatccta	aaaatcaaaa tagtagaaac	atactttaaa tatatacatt	540
gatcggacga aaattgtaaa	ctgtatgtt ttcaaaaaact	atgttgcacag gttatgtacc	600
ttaaacatTTt atttcaaaact	taaacactaa agaacatata	tgaatagaag tttatataaa	660
ttactatata tctaccataa	atctcttata attatgtat	cacgttgggg aagtgttgg	720
acgttaaaat gccaaaatat	aagcatgcg cggatTTT	gcagaagatt gttagtgt	780
aatctgtcgc aatcattact	cgtcttagca ttttcattt	tccttcattt tggataaac	840
gcacgtatata acattctaca	caccaacaag attctataaa	aacgcaaaagg ttgtctccat	900
agaatatcgt c			911

<210> SEQ ID NO 62
<211> LENGTH: 999
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0275

<400> SEQUENCE: 62

aaacattaat atgttagtaac	tatgggcgta tgctttactt	tttaaaatgg gcctatgcta	60
taattgaatg acaaggatta	aacaactaat aaaattgtag	atgggttaag atgacttatt	120
tttttactta ccaattata	aatgggccttc gatgtactga	aatatatcgc gcctattaac	180
gaggccattc aacgaatgtt	ttaaggccc tatttcgaca	ttttaaagaa cacctaggc	240
atcattccag aaatggatat	tataggattt agataatttc	ccacgtttgg tttatTTTC	300
tatTTTTGA cgTTGACCAA	cataatcgTG cccaccgtt	tcacgcaacg aatttatata	360
cggaaatataat atatTTTC	aattaagata ccacaatcaa	aacagctgtt gattaacaaa	420
gagatTTTT	ttttgggtt ttgagttaca	ataacgttag aggataaggt	480
gatTTTTGA	tcgtataaaa taaaatATGT	tataattaag tggTTTATTt tataatgagt	540
atTAATATAA	ataaaacCTG caaaaggata	gggatTTG ataataaaga gaaacgaaag	600
AGCAATTtTA	cttCTTTATA attgaaatta	tgtgaatgtt atgtttacaa tgaatgattc	660
ATCGTTCTAT	atattgaagt aaagaatgag	tttattgtgc ttgcataatg acgttaactt	720
CACATATACA	tttattacat aacatttac	acatgtgcgt ctTTTTTT ttttacttt	780
TAAAATTCC	tcactttaa gactttata	acaattacta gtaaaataaa gttgtttgg	840
GCTACACCCt	ttctccctcc aacaactcta	tttatagata acattatac aaaaatcaaaa	900
CATAGTCCT	ttcttctata aaggTTTTT	cacaaccaaa tttccattat aatcaaaaa	960

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ataaaaaactt aatttagttt tacagaagaa aagaaaaca	999
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<210> SEQ ID NO 63
<211> LENGTH: 981
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0285

<400> SEQUENCE: 63

gggattatat atgatagacg attgtatgg cggcacattg agatgttcc gaaaatagtc	60
atcaaatac aaaccagaat ttgatgtcaa aacactaatt aaaacatata attgacaact	120
agactatac atttgttaag ttgagcggtt aaagaaaatg aaagagtgtt gactgttagta	180
cgtatgagtt tccaaaaga tggtgcttga atattattgg gaagagactt tggtgggtc	240
ggttgaatga agattttac ctgccatgtt gatagagaaa ggcaaataaa tgttagggtc	300
gatgtctaac gtaaaagactg gatcaacca gagtcctcct cctcgtctc accaaaaaaaa	360
aagagtccct ctcgtggaaa cttatttctt ctccagccaa gatctcatct catctcttca	420
ctctatgaaa tataaaggaa tcttatggtt ttctaaaaaa ctatagtagc tctatataacc	480
aaaggaaaca atataaaatc agttaatctg ataaattttt agttaataat aaagttaact	540
ttgtacttac ctatataaaa ctaattcaca aaataaagta ataataacaa agaattttta	600
gtagatccac aatatacaca cacactatga gaaatcataa tagagaattt taatgattt	660
gtcttaactca tagcaacaag tcgccttgc cgagtggta aggcgtgtgc ctgctaagta	720
catgggctct gcccgcgaga gttcaaatct ctcaggcgac gtttctttt tttcggcca	780
taaaggaaaa agcccaatta acacgtctcg cttataagcc cataaagccaa acaatggct	840
gtctctgtct cactcacaca cgcgtttcc tacttttga ctattttat aaccggcggg	900
tctgacttaa ttagggtttt cttaataat cagacactct ctcactcggt tcgtcaacat	960
tgaacacaga caaaaccgcg t	981

<210> SEQ ID NO 64
<211> LENGTH: 996
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0286

<400> SEQUENCE: 64

aaaaacaatc ataggttacg ctattatcat cgaaaggat gtgatgcata ttcccatgt	60
accagatttc cataatatttt attgtaaag tgataatgaa tcacaagatg attcaatatt	120
aaaaatgggt aactcaactt gacgtgttagt acgtggaaga atagtttagt atcacgcata	180
catatatcta tgaataagt tttatgtacat aagaaactaa aatatttacc taaagtccag	240
ttactcatac tgatttcatg catatatgtt ttatttatattttaata aagaagcgat	300
tggtgtttc atagaaatca tgatagattt ataggttattt cagttccaca aatctagatc	360
tgtgtgttat acatgtatgtt attaattttt tcccccttaaa tcatttcagt tgataatatt	420
gctctttgtt ccaacttttag aaaaggtatg aaccaacctg acgattaaca agtaaacatt	480
aattaatctt tatatgagat aaaaccgagg atatatatgtt ttgtgttgat gtctattgtat	540
gatgtgtcga tattatgtt gttgtaccaa tgctcgagcc gagcgtgtac gatgccttga	600

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caaactatat atgttcccg aattaattaa gtttgtatc ttaatttagaa taacatttt	660
atacaatgta atttctcaag cagacaagat atgtatccta tattaattac tatatatgaa	720
ttgccggca cctaccagga tgtttcaa atcgagagccc attagttcc acgtaaatca	780
caatgacgcg acaaaaatcta gaatcgtgtc aaaactctat caatacaata atatatattt	840
caaggcaat ttgcacttct cctcaactca atgattcaac gccatgaatc tctatataaa	900
ggctacaaca ccacaaagga tcatcagtca tcacaaccac attaactctt caccactatc	960
tctcaatctc tcgtttcatt tcttgacgcg tgaaaa	996

<210> SEQ ID NO 65
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0337

<400> SEQUENCE: 65

taattttttt atttttggaa ctaacactta ttagtttagg tttccatcac ctatthaatt	60
cgttaattctt atacatgcat ataatacgaga tacatatata caaatttatg atcatttttg	120
cacaacatgt gatctcatc attagtagatgc attatgcgaa aacctcgacg cgcaaaagac	180
acgtaatagc taataatgtt actcatttat aatgattgaa gcaagacgaa aacaacaaca	240
tatatatcaa attgtaaact agatatttct taaaagtgaa aaaaaacaaa gaaatataaa	300
ggacaatttt gagtcagtct cttaatatata aaacatatac acataaataa gcacaaacgt	360
ggttacctgt cttcatgcaa tgtggacttt agtttatcta atcaaaatca aaataaaagg	420
tgtatagtt ctgcgtatc ttcaaattttt aaaaatcaga accaagtgtat ttttggta	480
gtattgtatcc attgtttaaa caatthaaca cagtatatac gtctcttgag atgttgacat	540
gtatgataaaa tacgagatcg tctcttggtt ttcaatttttaat gaactttaat agtttctt	600
tttagggaaa ctttaatagt tggttatcat aagattagtc acctaattgt tacgtgcag	660
taccgaacca attttttacc ctttttcttca aatgtggtc tggcataatt tccaaagag	720
atccaaaacc cgggttgctc aactgataag cccgtcggtt ctgggttggaa aaacaagaaa	780
taatctgaaa gtgtgaaaca gcaacgtgtc tgggtgtttc atgagccacc tgccacccca	840
ttcacgtcgg tcattttgtc gttcacggt tcacgctcta gacacgtgtct gtccccac	900
catgactttc gtcggcact cgcttcgtt tggaaactca aacatgtgt tatatgtaa	960
ttccatccta ataagcatct cttaccacat taattaaaaa	1000

<210> SEQ ID NO 66
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0356

<400> SEQUENCE: 66

ttagttcatt gaaacgtcaa ctttttactt gcaaccactt tggtaggacca ttaactgcaa	60
aataagaatt ctctaagctt cacaagggt tcgtttggtg ctataaaaac attgttttaa	120
gaactggttt actgggtctt taaatctata aatccaaata tgaagtatgg caataataat	180
aacatgttag cacaaaaat actcattaaa ttcctaccac aaaaaatct ttatatgaaa	240
ctaaaaactta tatacacaat aatagtgata caaagttaggt cttgatattc aactattcg	300

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gattttctgg tttcgagtaa ttgcgtataaa aggtttaaga tctattatgt tcactgaat	360
cttaacttg ttttgttcc agtttaact agtagaaatt gaaatttttta aaaatttta	420
cttacaataa aatttgaatc aatatcctta atcaaaggat cttaaagacta gcacaattaa	480
aacatataac gtagaatatac tgaataact cggaaatatac tgaactaagt tagtagttt	540
aaaatataat cccggtttgg accgggcagt atgtacttca atacttgttgg gttttgcga	600
ttttggatcg gattggcgcc gccagccaga ttgtatcttta acaaatttca cctgtcaacg	660
ctaactccga acttaatcaa agattttagt ctaaggaaaa ctaatcagt atcacccaaa	720
gaaaacattc gtgaataatt ttggctttc catggcagca aaacaaatag gacccaaata	780
ggaatgtcaa aaaaaagaaaa gacacgaaac gaagtagtat aacgtaacac acaaaaataa	840
actagagata taaaaaacac atgtcccacac atggatacaa gggcatttaa ggagcagaag	900
gcacgtatgt gttagaaggt atgtgatata attaatcgcc ccaaataatgat tggtaagtag	960
tagccgtctt tatcatccat actcatcata acttcaacct	1000

<210> SEQ ID NO 67
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0374

<400> SEQUENCE: 67	
aagacacccg taaatgttgcatgtagaag aaactagaaaa cgttaaacgc atcaaataa	60
gaaaattaaat tgaaggtaat tttaacgcgc gcctttcaaa tattttcttctt aggagaggct	120
acaagacgcg tattttttc gaattctcca aaccattacc attttgcata ataatccga	180
catgccgttg ataaagtttgc tatgcaatc gttcattggg tatgagcaaa tgccatccat	240
tggttcttgc tattaaatgg tccaaaaataa gtttggccc actactatgtt actattttgt	300
atcactctgc aaaataatca tgcataaaac gttatgtgcata tttctaaatataa aaactcaaaa	360
gtaatcaatgc tacaatgcag agatgaccat aaaagaacat taaaacacta cttccactaa	420
atctatgggg tgccttggca aggcaatttgcataaggagaaa tgcataaga tgatataagaa	480
aatgctattc agtttataac attaatgttt tggcgaaaaa ttttctatattt attagacctt	540
tctgtaaaaa aaaaaaaaaatg atgtagaaaaa tgctattatgtt tttcaaaaat ttcgcactag	600
tataatacg aacattgttag ttacactgc tcattaccat gaaaaccaag gcagtatata	660
ccaaacattaa taaactaaat cgcgatttctt acgcacccca ttaattaatt ttactattat	720
acattctctt tgcttctcgaa aataataaac ttctctatattt cattctacat aataaataag	780
aaagaaaatcg acaagatcta aatttagatc tatttagttt tttcgcttgc gaagccaaaa	840
ttgtgtatgc aagaaagcag tgcgtatctt cccacgttttgc gacgaaataa aacataacaa	900
taataaaata ataaatcaaataatc cctaaattttgtt cttttattact ccacaatttt	960
ctatgtatgc atatataaccc acctctctct tgcgtatcttgc	1000

<210> SEQ ID NO 68
<211> LENGTH: 998
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0377

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<400> SEQUENCE: 68

tataaacat tcctataaca ccataattaa acataacaat gaattgcttg gatttcaaac	60
tttattaaat ttggatttta aatttaatt tgattgaatt ataccccctt aattggataa	120
attcaaatat gtcaactttt ttttgttag attttttat ggaaaaaaaaa attgattatt	180
cactaaaaag atgacagggtt acttataatt taatataatgt aaaccctaaa aagaagaaaa	240
tagttctgt ttcacttta ggtcttatta tctaaacttc tttaagaaaa tcgcaataaa	300
ttggtttgag ttcttaactt aaacacatta atatttgtgt gctatttaaa aaataattta	360
aaaaaaaaa aacaaattga cagaaaatat caggtttgt aataagatat ttccgtataa	420
atatttaggg aatataacat atcaaaagat tcaaattctg aaaatcaaga atggtagaca	480
tgtgaaagtt gtcatcaata tggccactt ttcttgctc tataacccaa aattgaccct	540
gacagtcaac ttgtacacgc ggccaaacct tttataatc atgctattta ttcccttcata	600
tttattcta tttgtatct aactgatttt tcattaacat gataccagaa atgaatttag	660
atggattaat tctttccat ccacgacatc tggaaacact tatctctaa ttaaccttac	720
tttttttta gtttgtgtgc tccttcataa aatctatatt gttaaaaca aaggtcaata	780
aatataaata tggataagta taataaatct ttattggata ttctttttt taaaaaagaa	840
ataaatctt ttggatatt ttctgtggcag catcataatg agagactacg tcgaaaccgc	900
ttggcaaccac ttgtggcgcg tttaatttct ttctgaggct tatataaata gatcaaaggg	960
gaaagtgaga tataatacag acaaaacaag agaaaaga	998

<210> SEQ ID NO 69

<211> LENGTH: 999

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0380

<400> SEQUENCE: 69

acaagtgacca ttcactttt tactttcaa tgtatacat catcatgtgaaaaaaaaaa	60
aatgtAACCA atcaacacac tgagatacgg ccaaaaaatg gtaatacata aatgtttgt	120
ggttttgtaa tttaaatact tttagttaagt tatgattttt ttatTTTGC ttatcactta	180
tacgaaatca tcaatctatt ggtatcttt aatcccgtt tttaatttcc accgcacacg	240
caaatcagca aatggttcca gccacgtgca tttgaccaca tattgtggtc acagtactcg	300
tcctttttt ttcttttgc atcaataat ttcaatccta aaacttcaca cattgagcac	360
gtcggcaacg ttagtccta aatcataacg agaaaaaaatg ttcaaaattttt ggttatatgt	420
caattgatca tcaactacatg tctacataat taatatgtat tcaaccggc ggTTTGTGA	480
tactcatatg taagtataat tttgtgtattt agaatttagga tgaatcaggtt ctgtcaaaaca	540
actacggttt cataataatg gggagtgtt ttttacaaat gaaagaggat ggatcatct	600
gagatgttat gggctccag tcaatcatgt ttgtctcgca tatgctatct ttgtatctc	660
ttcctaaact catagaataa gcacgttggt ttttccacc gtcctctcg tgaacaaaag	720
tacaattaca ttttagcaaa ttgaaaataa ccacgtggat ggaccatatt atatgtgatc	780
atattgttg tcgtcttcgt ttcttttaa atgtttacac cactacttcc tgacacgtgt	840
ccctatttcac atcatccctt ttatatacgat ttacttataaa aggatcacga acaccaaaac	900
atcaatgtgt acgttttttgc cataagaaga aacagagagc attatcaattt attaacaatt	960

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acacaagaca gcgagattgt aaaagagtaa gagagagag	999
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<210> SEQ ID NO 70
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0381

<400> SEQUENCE: 70

cacggtaaa gtattgctaa catggcatt acattgaaaa agaaaattaa ttgtcttac	60
tcatgtttat tctatacaaataaaaaatatt aaccaaccat cgcactaaca aaatagaat	120
cttattctaa tcacttaatt gttgacaatt aaatcattga aaaatacact taaatgtcaa	180
atattcgttt tgcatatctt tcaatttaaa tacatttaaa gttcgacaag ttgcgtttac	240
tatcatagaa aactaaatct cctacccaaag cgaaatgaaa ctactaaagc gacaggcagg	300
ttacataacc taacaaatct ccacgtgtca attaccaaga gaaaaaaaaa gaagataagc	360
ggaacacgtg gtagcacaaa aaagataatg tgatttaat taaaaaaca aaacaaagac	420
acgtgacgac ctgacgctgc aacatcccac cttacaacgt aataaccact gaacataaga	480
cacgtgtacg atcttgttctt tggtttctcg atgaaaacca cgtgggtgct caaagtctt	540
gggtcagagt cttccatgtat tccacgtgtc gttatgcac caaacaaggg tactttcggt	600
attttggctt ccgcaaatta gacaaaacag cttttgttt gattgatttt tctcttcct	660
ttttccatct aaattctctt tggctctta atttctttt gagtgatcgatc tcgagattt	720
tccggatattttt ttcggtaaa tggtgaaatt ttgtggatt ttttttatt tcttttattaa	780
actttttttt attgaattta taaaaaggaa aggtcgatcat taatcgaaga aatggaatct	840
tccaaaattt gatatttgc tggttcttgg ggatttgaat tgctcttat catcaagaat	900
ctgttaaat ttctaatactaaatcta aatctaagt tgagaaaaag agagatctct aatthaaccg	960
gaattaaat tctccgaccg aagtattat gttgcaggct	1000

<210> SEQ ID NO 71
<211> LENGTH: 999
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0384

<400> SEQUENCE: 71

tttaaaaaat tggataaaac accgataaaa attcacattt gcaaattttt ttcagtcgga	60
atatatatattt gaaacaagtt ttgaaatcca ttggacgattt aaaaattttt gttgagagga	120
taaatatgga tttgttcatc tgaaccatgt cgttgattt gatggacta ccatgaaaaa	180
tatgttatgaa aagtataac aacttttgcattt aatcacattt tattaaacaat aatcaagac	240
aaaatatgtc aacaataata gtagttagaa atattaattt aatttcattt gtaacaacaa	300
aaaatcatac cacaattaag tgcacagaaa aaccttttgcattt tgcgtttt	360
caatgattttt cgtgaaaagg atatattttt gtaaaaataag aaggatcttgc acgggtgtaa	420
aaacatgcac aattcttaat tttagaccaat cagaagacaa cacgaacact tcttttattt	480
aagctttaaa aaaaaatctt gccttttgcattt ctttagataata tattttttt gactcatcg	540
ggagtgaaaa atatctcagg atttgctttt agctctaaca tgtcaacta tcttagatgcc	600
aacaacacaa agtgcaaattt ctttaatata gaaaacaaca ataatatttc taatagaaaa	660

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ttaaaaaggg aaataaaata tttttttaaa atatacaaaa gaagaaggaa tccatcatca	720
aagtttata aaattgtaat ataatacataa cttgtttgt tccttgtctc tccctgttc	780
tctctcatct ctccatctt ctccatataat acttcatactt cacacccaaa actccacaca	840
aaatatctct ccctctatct gcaaattttc caaagttgca tcctttcaat ttccactcct	900
ctctaataata attcacatatt tcccactatt gctgattcat tttttttgt gaattatssc	960
aaacccacat aaaaaatct ttgtttaat taaaaacca	999

<210> SEQ ID NO 72
<211> LENGTH: 998
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0385

<400> SEQUENCE: 72

actcaacaat aggacaagcc aaaaaattc caattattgt gttactctat tcttctaaat	60
ttgaacacta atagactatg acatatgagt atataatgtg aagtcttaag atatttcat	120
gtgggagatg aataggccaa gttggagtct gcaaacaaga agctcttgag ccacgacata	180
agccaagttg atgaccgtaa ttaatgaaac taaatgtgtg tggttatata ttagggaccc	240
atggccatatacacaatttt tggttctgtc gatagcatgc gtttatataat atttctaaaa	300
aaactaacat atttactgga tttgagttcg aatattgaca ctaatataaa ctacgtacca	360
aactacatata gtttatctat atttgattga tcgaagaatt ctgaactgtt ttagaaaatt	420
tcaatacact taacttcatac ttacaacggt aaaagaaatc accactagac aaacaatgcc	480
tcataatgtc tcgaaccctc aaactcaaga gtatacatt tactagatata gagaatttga	540
tatcctcaag ttgccaaaga attggaagct tttgttacca aacttagaaa cagaagaagc	600
cacaaaaaaaaa gacaaaggaa gttaaagatt gaagtgtatgc atttgtctaa gtgtgaaagg	660
tctcaagtct caacttgaa ccataataac attactcaca ctccctttt ttttctttt	720
ttttccaaaa gtaccctttt taattccctc tataaccac tcactccatt ccctctttct	780
gtcactgatt caacacgtgg ccacactgat gggatccacc tttcctctta cccaccccc	840
ggtttatata aacccttcac aacacttcat cgctctcaa ccaactctct cttctcttt	900
ctctcctctc ttctacaaga agaaaaaaaaa cagagcctt acacatctca aaatcgaact	960
tactttaacc accaaataact gattgaacac acttgaaaa	998

<210> SEQ ID NO 73
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0396

<400> SEQUENCE: 73

catagtaaaa gtgaatttaa tcataactaag taaaataaga taaaacatgt tatttgaatt	60
tgaatatcgt gggatgcgtt ttcggatt tgattaaagg tctggaaacc ggagctctca	120
taacccgaat aaaaatgcat aacatgttct tcccccaacga ggcgagcggg tcagggcact	180
agggtcattt caggcagctc ataaagtcat gatcatctag gagatcaaat tttatgtcg	240
ccttctcaaa attacctcta agaatctaa acccaatcat agaacctcta aaaagacaaa	300

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gtcgtcgctt tagaatgggt tcggtttttg gaaccatatt tcacgtcaat ttaatgttta	360
gtataatttc tgaacaacag aattttggat ttatggcac gtatacaa atctaattaa	420
taaggacgac tcgtgactat cttacatta agttcactg tcgaaataac atagtacaat	480
acttgcgtt aattccacg tctcaagtct ataccgtcat ttacggagaa agaacatctc	540
tgttttcat ccaaactact attctactt tgtcttatata tttaaaatata agtaaaaaag	600
actcaatagt ccaataaaaat gatgacccaa tgagaagatg gttttgtgcc agattttagg	660
aaaagtgagt caaggttca catctcaat ttgactgcat aatctcgcc attaacaacg	720
gcattatata tgtcaagcca atttccatg ttgcgtactt ttctattttagt gtgaaaatata	780
gggtttgtt attaatcaaa gagtttgct aactaatata actacgactt tttcagtgac	840
cattccatgt aaactctgct tagtgttca ttgtcaaca atattgtcgt tactcatata	900
atcaaggaaa aatatacaat tgtataattt tcttataattt taaaattataat tttgatgtat	960
taccccttta taaataggct atcgctacaa caccaataac	1000

<210> SEQ ID NO 74

<211> LENGTH: 1514

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter p13879

<400> SEQUENCE: 74

tttcgatcct cttttttttt aggtttcttg atttgatgtat cgccgcgcagt agageccgtcg	60
tccggaaatttt cagagattaa aaccatcacc gtgtgagttt gtagcgaatt aacggaaagt	120
ctaaatgtcaag attttttaaa aagaaattta tgggtgaaaaa gaagccgtt gttatattta	180
tataatttag aaaatgttcc atcattttaa ttaaaaattt aataatttgtt agaagaaga	240
agcatttttt atacataaaat catttaccc ttactgttgc tttttttca cttaatttcat	300
ttttactttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	360
taaaatggca tatgtttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	420
tcacaaaaaaaaa ccctagctaa ctaaagacgc atgtgttctt cttttttttt tttttttttt tttttttttt	480
tgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	540
taaaaggaa catgaagaac ttgagaccat gttttttttt tttttttttt tttttttttt tttttttttt	600
taactaaaga tacatttagat ggctttttttt tttttttttt tttttttttt tttttttttt tttttttttt	660
aaatcccttg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	720
gttgggtttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	780
tttgggtttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	840
tatcgacaaa aaaaaaaaaatgtt agtgggtttttt tttttttttt tttttttttt tttttttttt tttttttttt	900
catgcacatgc actaaggatgc aacaaaggatgc atatggccgc gttgggtttttt tttttttttt tttttttttt	960
taagggtttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	1020
aaatccatgc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	1080
taaaatagggg actagccgaa ttgatccggc ccagttatcg ttgtgtatca ccacgttatt	1140
tccaaatttca aactaaggggaa taaagatgtc atttgcata tttttttttt tttttttttt tttttttttt	1200
ctggatattttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	1260
ttggcgatattttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	1320

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cagatttaac catggtaaaa ccagaattca cgtaaacgga ctctaaacct agaaaatatc	1380
taaaccttgg ttaatatctc agcccccta taaaataacga gacttcgtct acatcggtct	1440
acacatctca ctgctacta ctctcactgt aatcccttag atcttcttt caaatttcac	1500
cattgcactg gatg	1514

<210> SEQ ID NO 75
<211> LENGTH: 1954
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter p326

<400> SEQUENCE: 75	
gtgggtaaaa gtatccttct ttgtgcattt ggtatTTTA agcatgtaat aagaaaaacc	60
aaaatagacg gctggtattt aataaaagga gactaatgtt tgtatagtat atgatttg	120
tggaaataaa taaaggTgtt aaatatacatgtt gtgaagcgag tatcttatTTTttca	180
aagggtatcg atcgTgttct ttgtgatagt ttggTcgTc ggtctacaag tcaacaacca	240
ccttgaagtt ttcgegtctc ggTTTCTCT tcgcatacggtt tatccaatag catacatata	300
ccagtgcggaa aatggcgaa gactagtggg cttgaaccat aaggTTTggc cccaatacgg	360
attccaaaca acaagcctag cgcaatTTT tcggatgtt aagactaaac tgTcgactgt	420
atagacgtaa gatataatcga cttgatttggaa atcgTctaag ctaataagtt tacTTtgacc	480
gtttatagtt gcgtcaacgt ccttatggag attgtatGCCc atcaaataaa cctgaaaatc	540
catcaccatg accaccataa actcccttgc tgccgctgtt ttggcttggag caaggTTTT	600
ccttgcggaa ctccgcattt tggataaaagt gttccacttt ttgcaagttag ctctgacccc	660
tctcagagat gtcaccggaa tcttagacag aaccccttctt gccaatcac ttggaaagatc	720
ggacaatgtc atcatttttgc caggtaattt ctccttgcgtt gtcgtttgg cttggacacg	780
gtgcttcttt gtaaaagctcc gatTTTggaa taagagcgga tcggaaatctt cttaggggtt	840
ccagTCCTT gacctattaa tttatagaag gtttttagttt atttttttcc aatttcttct	900
ctaacttaac aaataacaac tgcctcatag tcattggctt caaatTTTat cgcttgggtt	960
atTCGTTT ttgcaaggcc ttggcccatt ttgagccaa taactaaatc tagcTTTtc	1020
agacccggaca tgaacttcgc atattggcgt aactgtgcag ttttaccttt ttccggatcat	1080
acaagatcg atttagacca cccaaacaata gtcagtcata ttgacaacc taagctagcc	1140
gacactacta aaaagcaaac aaaagaagaa ttctatgttgc tcattttacc ggtggcaagt	1200
ggaccCTTCTT ataaaagagt aaagagacag cctgtgtgt tataatctctt aattatgttc	1260
accgacacaa tcacacaaac ccttctctaa tcacacaaact tcttcattgtt ttacgacatt	1320
aattatcatt aactctttaa attcacttta catgctcaaa aataatctaattt ttgcagcatt	1380
aatttggatca cctgataacta ttattataat cgtcgtgattt cgcaatcttc ttcatTTT	1440
gctgtcaagt tgcgtcgca cgcggggc cagtgaaagca aatccaaacgg tttaaaacct	1500
tcttacattt ottagatctaa tctgaaccgtt cagatatactt gatcttcatgtt tctgaacaca	1560
gttagatgaa actggaaatg aatctggacg aaattacgtt cttacaccaa cccccctcgac	1620
gagctcgat atataaagct tatacgctcc tccttcaccc tgcgtactactt actaccacca	1680
catttcttta gctcaacctt cattactaat ctccTTTaa ggtatgttca ctTTTCTTcg	1740
attcataactt tctcaagattt cctgcatttc tgcgtttttttt gaaaccaagtg tcgatTTT	1800

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tttgagagaa	gtgttgcatt	atagatctgg	ttattgaatc	tagattccaa	tttttaattg	1860
attcgagttt	gttatgtgtg	tttatactac	ttctcattga	tcttggggta	tttctctgct	1920
ctgttattagg	tttctttcgt	gaatcagatc	ggaa			1954

<210> SEQ ID NO 76						
<211> LENGTH: 2016						
<212> TYPE: DNA						
<213> ORGANISM: Arabidopsis thaliana						
<220> FEATURE:						
<221> NAME/KEY: misc_feature						
<223> OTHER INFORMATION: Ceres Promoter p32449						
<400> SEQUENCE: 76						
gatcgccctt	tttcaggctt	tctctgttagc	tctgttactt	catacacagt	tatcggttat	60
ttgagaaaaaa	agagtttagct	aaaatgaatt	tctccatata	atcatggtt	actacaggtt	120
tacctgattc	gcgttagctt	tatctgcatac	caaagttttt	tccatgtatgt	tatgtcatat	180
gtgataaccgt	tactatgttt	ataactttat	acagtctggt	tcactggagt	ttctgtgatt	240
atgtttagta	catactcatt	catactttgg	taactctcaa	gtttaggttg	tttgaattgc	300
ctctgttgtt	atacttattt	tctattgtat	caatcttcta	atgcaccacc	ctagactatt	360
tgaacaaaga	gtgtttcat	tcttaaacct	ctgtgtctcc	ttgctaaatg	gtcatgctt	420
aatgtcttca	ctgtctttt	tcttctatag	atatgtatgc	ttgcttagata	gttagttcta	480
cagctcttctt	ttgttagtctt	gttagagagt	tagttgagat	attaccttctt	aaaagtatcc	540
ttgaaeegctt	tcgggttatg	accattttgt	tgtagctctt	tgtaaatgaga	acttactggg	600
accagegaga	cagtttatgt	gaatgttcat	gtttaagtgt	cgaacgtatc	tatctctact	660
atagctctgt	agtcttggta	gacagttatgt	tttataatctc	catttttttg	tagtcttgct	720
agtttagata	ttacctcttc	tcttcaaagt	atccttgaac	gttcaccgg	tatgaaatct	780
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tagttcttta	gtctccctt	tgttagcctt	ctacagagta	agatgggata	ttacctcttt	900
gaacgtctc	cgttatgtac	caatttgg	tagtccctt	taagtagaaac	tttaggataga	960
gtgagtcaac	ttaagaaag	aacctagttat	gtggcataac	cagattgcag	gtctgtctc	1020
ggctacagta	acgttaactct	atagctcttt	gttttgttca	gaaagaacca	gtgattggat	1080
gatcgtcct	tagaaactgg	acctaacaac	agtcattggc	tttgaatca	agccacaaca	1140
atgcctatat	gaaccgtcca	tttcatttat	ccgtttcaa	ccagcccatt	acattcgtc	1200
ccattgataa	ccaaaagcgg	ttcaatcaga	ttatgtttta	attttaccaa	attctttatg	1260
aagtttaat	tatactcaca	ttaaaaggat	tattggataa	tgtaaaatt	ctgaacaatt	1320
actgattttg	gaaaattaac	aaatattttt	tgaatataaa	gaaaagcct	tttccctttt	1380
gacaacaaca	tataaaatca	tactcccatt	aaaaagattt	taatgtaaaa	ttctgaatat	1440
aagatatttt	ttacaacaac	aaccaaaaat	atttattttt	ttcccttttt	acagcaacaa	1500
gaaggaaaaa	ctttttttt	tgtcaagaaa	aggggagatt	atgtaaacag	ataaaacagg	1560
gaaaataact	aaccgaactc	tcttaattaa	catcttcaa	taaggaaaat	tatgtccgc	1620
atatttagga	agatcaatgc	ataaaaacaa	cttgcacgtg	gaaagagaga	ctatacgtc	1680
cacacaagtt	gcactaatgg	tacctctcac	aaaccaatca	aaatactgaa	taatgccaac	1740
gtgtacaaat	tagggtttt	cctcacaacc	atcgaacatt	ctcggaaacat	ttttaaacagc	1800
ctggcgccat	agatctaaac	tctcatcgac	caattttga	ccgtccgatg	gaaactctag	1860

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cctcaaccca aaactctata taaagaaatc	tttccttcg ttattgctta ccaaatacaa	1920
acccttagccg ccttattcggt	cttcttcgtt ctctagttt ttccctagtc tctgttctta	1980
gatcccttgt agttccaaa tcttccgata aggct		2016

<210> SEQ ID NO 77
<211> LENGTH: 667
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PD1367

<400> SEQUENCE: 77

acagtttct tttctcatct tacaacaagt ttccaggagg atagagacat aaacgaagct	60
cggattgtat cgttttttt agcttttatt cacatccgaa agtcctgttag ttttagattct	120
gttatcttcgc ggttttgagt taatcagaaa cagagtaatc aatgtatgt tgccaggctag	180
atctttcatc ttggaaatt ttttttttc tcatgcaatt tcttttagctt gaccatgagt	240
gactaaaaga tcaatcagta gcaatgattt gattggota agagacattt gtccacttgg	300
catcttgatt tggatggta caacttgcaa gacccaattt gatacttgcg atgacaactc	360
caactcaaga gtgtgtgtta actaagaacc ttgactaatt tgtaatttca atcccaagtc	420
atgttactat atgtttttt gtttgatatttttttcttcc tacaattaag ctctttgacg	480
tacgtaatct ccggAACCAA ctcctataatc caccattac tccacgttgt ctccaaattat	540
tggacgttga aacttgacac aacgtaaacg tatctacgtt gttgattgtt tgtaatatttgc	600
tacaaacgtt cactttctc ctctttcaat tcatacttgc gttgtgaat tcattaaatc	660
ctgcgaa	667

<210> SEQ ID NO 78
<211> LENGTH: 252
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PD0898

<400> SEQUENCE: 78

cgcaggccccg atcggcctaa ataattatag tcataagagg acccaaataa ataaataatg	60
ggattctctg aggtgtatTT ttttatgcac acgtaaaacg gtgaaagatt tgtaaaccta	120
ctttatatat atacttccat ctctttgtct ttgttacaat ttgaatcaga gagaaattaa	180
gaagcgaaaa acaaagaacg agaggaggcg agaggtatag aagaatattc cttgtggccg	240
geaaggccaa tc	252

<210> SEQ ID NO 79
<211> LENGTH: 283
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter PD0901

<400> SEQUENCE: 79

caaagtattt gacaagccat atgggtttgg atcaaaaagt cggccaaaa ttaatgtttt	60
atgtgcaaga accgaccat tgcacacacg ttttacatc ttcaagactt tcatctctat	120
ttttcttttg gtcattaaga tacccattga tccgaatctg ttacattccc acctactttt	180

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ttaatttta ctatccactc caaattaaac acaaccgatg attttaataa ttggaagctt	240
ttaaaatat ttctccacgt gcctctttgt gtttgtctat ata	283
<210> SEQ ID NO 80	
<211> LENGTH: 999	
<212> TYPE: DNA	
<213> ORGANISM: Arabidopsis thaliana	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<223> OTHER INFORMATION: Ceres Promoter YP0022	
<400> SEQUENCE: 80	
tagttccatt acaatttcca aatgatttg tacaagcta caagattatt cgaaatagga	60
tttcatccat aagagagaat ggtgtggcgt acgctacaat gttgatttat tggttggt	120
ttgcacatcg gggatgtcaa atcctaagtt tcaagttctt gtaaaaacgt tttcagggtt	180
cttaaatata tttaatatt aatgtaaaaa gaaaagatat agctttgtt caaaaaaatt	240
tgttaatca ctatgttagg ggtgcgtat aaattcatgg aatgtatgtat tattagctt	300
tctatccatca ctctaaaaac aatactatag tgagttaat aatttgcata tttcaatgtt	360
gattaaaatt ttataaaag aaaaaatt taaaagcata taacaaaata aaaaaggagg	420
ctcgaggat gatgggtgtt gcagaagagc tggcaacagc tatcgactga gtgattacga	480
actcagtaat cagtgttctc agtcacaca ctctttttt gttcttttc tttggacag	540
ctttcatttt ctctttctt ttttctattt tgttcaaaa ttccatccat attaaaatag	600
gcctgatcat gagaataaaag gaaataactaa tggatgtttt ctcaataatg caataagatg	660
caattattat gagctattta ctattgaaaa tgagcaataa aatgtcaaaa cacaatctgg	720
ttaagttaga gcaactccat tggatgttgc tcatgttagt tctaaagaaaa caaaaatgtat	780
taatatttta cttttacatc caaaaaacca acttataatgc gtaatagaaaa cgatccta	840
attaggaatt ttagagattt tctctcatct gtttcttaac ttttcaatat ttttattttt	900
taaaattgtt ttagtttcta ctaagaaact actgctggag ttggctttag ctcccata	960
cttctccacc tatataatgc cataatctct tcttaaaac	999
<210> SEQ ID NO 81	
<211> LENGTH: 999	
<212> TYPE: DNA	
<213> ORGANISM: Arabidopsis thaliana	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<223> OTHER INFORMATION: Ceres Promoter YP0080	
<400> SEQUENCE: 81	
aagcggcaat ttagtaagaa gtactcaaag tatcatttac caaaaagtata tggtttggg	60
aagagttgtt agggatgtat tctttctaaa cagatgtat gacgtgttc ttgaaaacta	120
atgttaaaga cggaaatctct ggcatttca ctcggagat atattaaacc gttgttgta	180
gttagccatg tacttagctt agtgcacaaa taatctgtt caagaaatct ttttctatta	240
taatatctct catttaaaca ttagaacata ttgtttaact tggcttctt gaaataaaac	300
tgctaatttc ttatggtaaa ctatttctt ttagattgca caatcgaaact cgaaaatcta	360
gtggagacta tggactatg tttatataa tggaaacctaa atcaaattat cccataatt	420
gggagacaca aaagaaaaat tacgaaagaa aacaggaaat caaatcaaaa gataaagaga	480
aggtaaaaaa aggcaagaag cactaatgtt taatattat agtttctcc attaaagaaa	540
aagcgatgtat gtgtgttctc atctttgtt aaagttataa tattgtttt gctttctca	600

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aaagcaaaaag actcatccaa caagaacaaa aaaaaaaact aaagctaat ccaaaagacg	660
aagaatgcattggatactac aacttcttt tcactttct ttcaaattta caattatgat	720
tttcacaata cagtttattc aaaaataat aaaaaacga ggcataaaaa taatgattat	780
cctcttcaact tattaagcca ctcactataa gcagagcaac tccagaacat agtgagcccc	840
caaaacatta aagcatgatg atgtctaattg atgtatgtatct tcttcgttcc atttctctaa	900
atttttggaa ttctcgaa gacccttctt ctcttctct tctctgaact tcaagattcg	960
tgtcgacaa atttttgttt ttatTTTCTT gatgttaca	999

<210> SEQ ID NO 82

<211> LENGTH: 999

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0087

<400> SEQUENCE: 82

tgaattttagt aaaaatgtgtt ttcaaacagt taggtggtag aaggttaagg taataacatc	60
atgatcttac taaaagaatt gttgcataact aactatcaat attctcaaca acataatata	120
atgtttttt aggttaatttt ccattttat tttttgtat taaacaatata aacaactcga	180
atgatgtatgta taaaaaaaaaa aaattaacaa ctcgaataag ttaaagttagc aatacacatg	240
tcgttcaattt caaccaataa agtaagactt atatttttaa gaagttgact aatagctaa	300
taagttggaa aacttggatgtt gtttcttaat tcccacgtgc agtaagaaat aaaaatgaaa	360
aaaattatata tatccttccc actctgcgac ttttcttttta ttttatcaaa tattaaaaag	420
attcatatca cagtttacac attgaaatca taaacgataa ttatgtatattt tggataaaaa	480
agtttagttctt gaagctcata ctttggatag tcgctagtcg ctaatatgtct ctttgcataa	540
attaaagtca ctacgacgca cgtcaaaagcc gatattttagg gcttaatttga tgcgttttt	600
tcttttata taatagtaat ataaattatgt actaataaaag tatgtatggat gggtttagaca	660
gaaaagaaaa aagatgactg tatggatcata attacaaaga agaatgtattt cttcatgttc	720
ttaagaataa taaaatgtca cttgtaaatc aagttggtaa gcatttttagg aacttttttc	780
gatgcaacgt atgatgatattt atgttagacaa aagataaaac cgtatcttca actattgcc	840
agaaaaagata aaacctaatac tagtcagttt ctcacacataa atacaacccca atagccaaac	900
tgtgtccaaat tcggagagaa actaaactaa aacaaaacac aaaagccaa cataagccca	960
ataaaaacccca ttttataaac agaacattac taacactca	999

<210> SEQ ID NO 83

<211> LENGTH: 1000

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter YP0093

<400> SEQUENCE: 83

atgatgaaca ttctacataat ataattatata tgtttaagca ctttagacagc ataaatttctt	60
tctaattata taaatctaac cttgttacat tgtacatcta taaattactt gaagaataaa	120
cgagttctat ttctttttaa aaattaaaa tactatacca tatctcagtg attaagtgtat	180
acccaaaaggt acggaggaga aacaagcatt tgattcttcc ttatTTTATT ttattcatct	240

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ctcactaatg atgggtggaga aaaaaagaaa atacctaaca aacaaatata tattgtcata	300
caaaaatatt tctatattt tagttaatta gtttatcc ctcactttc agggctata	360
taagaaaatg agcaaaccaca aatcaaaaatg cagcagcaaa tactatcatc acccatctcc	420
ttagttctat ttataatc ctcttcttt tgttcatagc ttgttaatta tagtcttatt	480
tctcttaaag gctcaataag aggaggtaact attactacac ttctctctac ttttacttgt	540
attttagcat taaaatccca aaatccgtt taaaattcaaa aataaactta gagatgtta	600
atctcgattc gggttttcgg cttaggaga ataattatata gaaatttagta tggatatctt	660
tactagtttc cattcaaataatg attctgattt caatctaata ctctcactct ttaattaaac	720
tatatgtatgt gtaattcac actgttaat ttctaccatg tcatgtatata tagagttca	780
tagaaaaattt gaaaaacatcc atttgaattc gaatgaaaaca aaatgttttta aaataaaatt	840
ttggttttta aaagaaaaat ctaaaaactgta attatatacg ttaaccagg tggaaaaatgc	900
ataaaaacgta gtatcttgta aatcgctt ccacggtcca aatagacttc tagtaataaa	960
caagtaaaac taattttgggt ttcttactaa ttttcacaga	1000

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<210> SEQ ID NO: 84
<211> LENGTH: 999
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0108
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<400> SEQUENCE: 84

ttagtgaac caggaaatg atctttata ccagttccg ggtttagatt ggtttgatgg 60
cgatttattt gatcccccga aattttatgt cgtagtgtg catagtatta ttattttttg 120
cggacaatag acgtatcggg accaagttct gtagcaaat tgtataagct taagtttgc 180
gaaatttaaa ggttaatcact aaaacccaaa tgggacaata aaccggtgaa gatttagagt 240
ttttatattt gactcatgaa tctggagaaa gagcccttgt taaaaggagt gaatcaatcc 300
ataggggaaa aagttttgtc tttttaaaaa ctaaagaacc aaaccttaat agaagcagct 360
caatgtgtga caactttcca ctggcactaa gataaagtga cttagcgtga gtgcatttat 420
tgaaatagta gatggtaaat attacatatac agagtaaaaa tatctttatg tcaatgctta 480
attcagtgtt tctggtaaac aagagaaact tctctaactt tcgttaattgg gtcttataaa 540
attttatgca attatgattt tacccttttta ctactttca ttagcttca cgaatctatt 600
ttgacaagag aaatcattag aggttaacat gctttttgtt caagggcctt aacagttcca 660
ccaaatcaagc tcaaaagtgt tacttaaccg acatcttcgt tgaaaacata taattacatg 720
tacaaatcaa aactacctt tggaaataat agaaatattt cagttcattt ctaatttaac 780
ctcttcaact tttaaaactt tttacattt tttatgtcat ttcttagtcat ttttgatgcaa 840
attgttacat ttatggattt tcttcacaaa ttttaagttt ggtgaaaact ttttgggtggg 900
tagttaaaac ttgaaataga aatttacttt accaaaataa actaatgaaa agtaatcact 960
ccactccctttaataaaggat tccaaacgttc ccactaaac 999

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<210> SEQ ID NO 85
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres Promoter YP0388
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<400> SEQUENCE: 85

agaaggattc acgcaccaag gttatattt tagtgacata ttctacaatt atcacat	60
tctttatgt ttcgttagtcg cagatggta atttttcta taataattt tccttgaaca	120
cacccaaacct tagaaacgat gatatatacc gtattgtcac gtcacaatg aaacaaacgc	180
gatgaatcg catcaccagc taaaagccta aaacaccatc ttagtttca ctcagataaa	240
aagattttt gtttccaacc tttctattga attgatttgc agtgatgacg taatttgc	300
tagttttag taaaacaaat ggaagtggta ataaatttac acaacaaaat atggtaagaa	360
tctataaaat aagaggttaa gagatctcat gttatattaa atgattgaaa gaaaaacaaa	420
ctattggttt attccatat gtaatagtaa gttgtatgaa aagtgtatgac gtaatttagtt	480
gtatttttag taaaacaaat taaaatggta aggttaattt ccacaacaaa acttggtaaa	540
aatcttaaaa aaaaaaaaaaag agggttagag atcgcattgcg tgtcatcaaa ggttttttt	600
cacttttaggt ctgagtagtg tttagactttt attggatgcac gtaagtgttt cgtatcgca	660
tttaggagaa gtacgtttt cacgtggaca caatcaacgg tcaagattt gcgtccaga	720
tagaggagcg atacgtcacg ccattcaaca atctccctt cttcattcct tcattttgat	780
tttgagttt gatctgcccc ttcaaaaatgc tcggatcatct gcccgttaat ataaagatga	840
ttatattttt ttatatcttc tggtgaaaga agctaataa aagcttccat ggctaatctt	900
gtttaagctt ctttttctt tctctctctt gtgtctcggt cactagttt tttcgaaaa	960
agagtgtatgg agtgtgtttt ttgtatagtt ttgacgtca	1000

<210> SEQ ID NO 86

<211> LENGTH: 3000

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Ceres Promoter PR0924

<400> SEQUENCE: 86

atctataacg agttaacatg ttgccagttt gaatcaagaa gcttggatga tgaatgaatg	60
gatcggtttt tggtaacatt cttaaaattt tagtagagga gacagagaaa aaacatgata	120
agactttggt atttacaact tgacggagac aagacagtaa gccaaatctg tcacaaaaac	180
actcaaactc ttttctcagt gtttgagtt taaagagaga cttattcaact tccccttcg	240
taacacttat ttgtctccca accaaacagt ttctgtcctt tcccttgc tcccacgtgc	300
atctttatat ctcatgactt ttgcatttca gatcttgaat aatgtcttag tggatttagt	360
ttgttgcgg taaatttagt gaccgtttt ttcttataatt tggaaagatcg cgggatgaag	420
cagatactga gtttcagggc atacacaccc aatttggaaaa tcattgttag tccaaattca	480
cttaatctt gtttacaaaa aaattgtatct gaaaatgttg atgggataag taaaaatgt	540
agttttgcta gtagtcatga tataataata gcaaaaccag atcaattttg agcaaaagga	600
agaaacaaaa aacagatcga tcccacgacg aagactaagt gtaaagtgtt tcccacaaga	660
gccatatgga tatggccctt caactttaa agcccattac ttcaatggc gacccgacat	720
tacgcccacga gtagtcacgc acgcacgact ccgttcacgt gacattcaatc ttgatattc	780
cccttctact ctcttcgtct tgggtatctt aaaaaacatcg aagagaccaaa cctaaattca	840
tattaatata tggatatacgat ttcaatctca acagtcactt tcgtatcca aatccatatc	900
ttacgaaatt agttcttaat aaagggtgtt gattaatgtt taatattgtt ttaagagttt	960

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agacacagca tataacacctg taccaacagt gctttattct taaatggaaa caaaacatat	1020
gtcaaatgtca agcatacagc taaaatatca ttatctaata ttaaggtaa aacaagataa	1080
ttaaaaattt aaacaacacc atattttat agctttactt atcgatcttt tctagtcttc	1140
atggtaattt tggtgtttt tttgtttt aaatgaattt gggtcgacca gatagtctaa	1200
tatcagtttt taaacactgg ttttaataaa atcatatgtc ggcaattcaa cctgttacgt	1260
tgtatgattt tattcttagtc aaataggggg ggaggtacta gtcgttcaa ttatgttacg	1320
taatcaatcc aaagaaaacta taagctataa agatcctcaa tttgtgggtt acaataaaaa	1380
caacagttgtt caaaattttt gtttataaaa agtaataact atgttccttc ccataatagag	1440
caaagtacctt caggataggc aaaccgtact taatagccct tattcataat ttgatccac	1500
tcttccccac aaaattgca ctgatgaagt caatacttgtt atagtgtttc aagctataaa	1560
tgtcttagtga tagtttggtc tcttaaaagg ttaacaaaag ttatgacaag ctgaaaaatc	1620
agagtttgc aggagtattt cttacagtta tcagtttaag tattcacattt atatgtttgt	1680
atacaatgat tcttaaattt cacctttcc gtgcgaaacc aaattttcta ttggaaacat	1740
agaatgtaaa caaaatatg ggacgttgc cggttcaaca ttaaccaaac ttgtcttata	1800
ctaataattcg tggtggttt atgttggatg tcttaaattcg ttgaatcatg tgcgttgc	1860
cggaaatatgc atcttctt atctttagtat agatgcactt tatcattttt ttgttacatg	1920
cttaattttt tttttaaaa tatgttgatt gtcattttgc caaaagtatg aattaaagac	1980
gcacatctaa cacaagttttag cagccgtaaa tccttccata aattttttt gcaagtttgc	2040
ctcattatata aatgagcgg aattatgata taatcggtttaa ttataatgtt atgttttgc	2100
caaaatttgc aattaaatgtt aggtgagaac ttgttataaca gtgttagataa ggtggatctt	2160
gaatataaaa ataaaatttta taagatgtat ttaaagcaga aaagcataaa acttttagata	2220
aaataatgtt aaaaatgtt agcatcaatg ttggatatt ggccgaccgg aacttaatca	2280
atgtcggaaag ccattacttc tctccaaaaa gaccttttc ctgcggagaa ctggaaactt	2340
cctcaactacc ttccgtttaa cgtgaaagcc ataaattca tatattcata aaaatcagaa	2400
aatctaaaac tgtttagtat cacctgtttt tggtatagac tattgggttt gtgttaccc	2460
ctaaactata tgatttcgtt ctccattggta tcttataagat atgaatatttc gtaaaaagat	2520
aagttatctg gtgaaacgtt acttcagtca tggtgggtctt agatttacat actactatga	2580
aacattttaa gataataattt atccatggca actatatgtt ctatattatg ggccaaagaa	2640
atatagaact aaaagttcag aatttaacga tataaatttac tagtataatttc taatacttgc	2700
atgattactg tttagttgtt tttagataaaa tagtagcgtt tggtttaaga taccatctat	2760
ccacatctat atttgggtgg gttacataaa atgtacataa tattatatac atatataatgt	2820
atatttttgc taaagccata tattactctt tgacctctgc ccccattttcc ttttactata	2880
aataggaata ctcatgatcc tctaaatttgc caatcaacac caacgaacac aacctttcc	2940
aaagccaata ataaaagaac aaaagctttt agtttcatca aagacgaagc tgccttagaa	3000

<210> SEQ ID NO 87
<211> LENGTH: 815
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 28780
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 88

<400> SEQUENCE: 88

aactactaaa cactaaatta tcaatccgt ctcttctcaa	aaaaaaaaaaa tcgactctaa	60
aatcaaactc tctcaaagct ccccaaaaaa acccttagttc	tgaatggaat cggcgattc	120
cggacgatcc gatccggtaa aaggagacga cccgggtcca	tcttcgtct cttcaccacc	180
agctacacct agcaggtatg agtcacagaa gegacgegac	tggaacacgt tcttgagta	240
cctcaagaac cacaagccgc ctctcgctt gtcacggtgt	agcggagcgc atgtatcga	300
gtttctcaag tacctcgacc agttcggtaa gaccaaagtcc	cacgtggccg cttgcctta	360
cttcggccat cagcaacctc cgttccttg ctcatgcctc	ctcaagcaag cttggggatc	420
tctcgatgt ttgatcgac ggtttagatc	tgcttacgag gagaacgggt gacggccgaa	480
ttcttaacccg ttgcggcac gtgcggttcg gatttacttg	agggaaagtca gagagagtca	540
ggcaaaggct cgtgggattc cttacgagaa aaagaaacgg	aaacggccgc caactgtcac	600
caccgttaga gttgacgtcg cttttcgag acaaagtgc	ggagacccctt gtaacgtcgg	660
tgctccatct gttgccgagg ccgttaccgccc ttatataaa	tattatataa tattatagtt	720
ttcttgattt atgatataata tatacttac tctatgtatg	tatggaaactc acttcatctt	780
ttgttcctta gtacctaatt attaaatttt gttcc		815

<210> SEQ ID NO 88

<211> LENGTH: 196

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Ceres CLONE ID no. 28780

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (13)..(145)

<223> OTHER INFORMATION: Pfam Name: DUF640

Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 88

Met	Glu	Ser	Ala	Asp	Ser	Gly	Arg	Ser	Asp	Pro	Val	Lys	Gly	Asp	Asp
1								10						15	

Pro	Gly	Pro	Ser	Phe	Val	Ser	Ser	Pro	Pro	Ala	Thr	Pro	Ser	Arg	Tyr
														20	30

Glu	Ser	Gln	Lys	Arg	Arg	Asp	Trp	Asn	Thr	Phe	Leu	Gln	Tyr	Leu	Lys
														35	45

Asn	His	Lys	Pro	Pro	Leu	Ala	Leu	Ser	Arg	Cys	Ser	Gly	Ala	His	Val
														50	60

Ile	Glu	Phe	Leu	Lys	Tyr	Leu	Asp	Gln	Phe	Gly	Lys	Thr	Lys	Val	His
														65	80

Val	Ala	Ala	Cys	Pro	Tyr	Phe	Gly	His	Gln	Gln	Pro	Pro	Ser	Pro	Cys
														85	95

Ser	Cys	Pro	Leu	Lys	Gln	Ala	Trp	Gly	Ser	Leu	Asp	Ala	Leu	Ile	Gly
														100	110

Arg	Leu	Arg	Ala	Ala	Tyr	Glu	Glu	Asn	Gly	Gly	Arg	Pro	Asp	Ser	Asn
														115	125

Pro	Phe	Ala	Ala	Arg	Ala	Val	Arg	Ile	Tyr	Leu	Arg	Glu	Val	Arg	Glu
														130	140

Ser	Gln	Ala	Lys	Ala	Arg	Gly	Ile	Pro	Tyr	Glu	Lys	Lys	Arg	Lys	
														145	160

Arg	Pro	Pro	Thr	Val	Thr	Val	Arg	Val	Asp	Val	Ala	Ser	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

161**162**

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165	170	175
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Gln Ser Asp Gly Asp Pro Cys Asn Val Gly Ala Pro Ser Val Ala Glu		
180	185	190

Ala Val Pro Pro		
195		

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<210> SEQ ID NO 89
<211> LENGTH: 198
<212> TYPE: PRT
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Ceres CLONE 1073674
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(146)
<223> OTHER INFORMATION: Pfam Name: DUF640
    Pfam Description: Protein of unknown function (DUF640)
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
    at SEQ ID NO. 88

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<400> SEQUENCE: 89		
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Met Asp Ser Gly Ser Gln Arg Pro Gly Pro Val Ser Glu Gly Asp Pro			
1	5	10	15

Gly Pro Ser Ile Val Thr Pro Ser Ser Pro Pro Ala Thr Pro Ser Arg		
20	25	30

Tyr Glu Ser Gln Lys Arg Arg Asp Trp Thr Thr Phe Leu Gln Tyr Leu		
35	40	45

Lys Asn His Lys Pro Pro Leu Ser Leu Ser Arg Cys Ser Gly Ala His		
50	55	60

Ala Ile Glu Phe Leu Lys Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val			
65	70	75	80

His Val Ala Ala Cys Pro Tyr Phe Gly His Gln Gln Pro Pro Ser Pro		
85	90	95

Cys Ala Cys Pro Leu Lys Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile		
100	105	110

Gly Arg Leu Arg Ala Ala Tyr Glu Asn Gly Gly Arg Pro Glu Ser		
115	120	125

Asn Pro Phe Ala Ala Arg Ala Val Arg Ile Tyr Leu Arg Glu Val Arg		
130	135	140

Glu Ser Gln Ala Lys Ala Arg Gly Arg Pro Tyr Glu Lys Lys Lys Arg			
145	150	155	160

Lys Arg Pro Thr Thr Val Thr Val Arg Val Asp Val Ala Ser Ser		
165	170	175

Arg Gln Ser Glu Gly Asp Gly Cys Asn Ile Gly Asp Pro Ser Tyr Val		
180	185	190

Ala Glu Ala Val Pro Pro		
195		

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<210> SEQ ID NO 90
<211> LENGTH: 198
<212> TYPE: PRT
<213> ORGANISM: Brassica napus
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Ceres CLONE 1118987
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(146)
<223> OTHER INFORMATION: Pfam Name: DUF640

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Pfam Description: Protein of unknown function (DUF640)
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88

<400> SEQUENCE: 90

Met	Glu	Ser	Thr	Asp	Ser	Gly	Ser	Gln	Gln	His	Gly	Gly	Asp	Pro	Gly
1								10					15		

Pro	Ser	Ser	Val	Thr	Pro	Ser	Ser	Pro	Pro	Ala	Thr	Pro	Pro	Ser	Arg
								25					30		

Tyr	Glu	Ser	Gln	Lys	Arg	Arg	Asp	Trp	Asn	Thr	Phe	Leu	Gln	Tyr	Leu
								35				40		45	

Lys	Asn	His	Lys	Pro	Pro	Leu	Ala	Leu	Ser	Arg	Cys	Ser	Gly	Ala	His
								50			55		60		

Val	Ile	Glu	Phe	Leu	Lys	Tyr	Leu	Asp	Gln	Phe	Gly	Lys	Thr	Lys	Val
								65			70		75		80

His	Val	Ala	Thr	Cys	Pro	Tyr	Phe	Gly	His	Gln	Gln	Pro	Pro	Ser	Pro
								85			90		95		

Cys	Ala	Cys	Pro	Leu	Lys	Gln	Ala	Trp	Gly	Ser	Leu	Asp	Ala	Leu	Ile
								100			105		110		

Gly	Arg	Leu	Arg	Ala	Ala	Tyr	Glu	Glu	His	Gly	Gly	Arg	Pro	Asp	Ser
								115			120		125		

Asn	Pro	Phe	Ala	Ala	Arg	Ala	Val	Arg	Ile	Tyr	Leu	Arg	Glu	Val	Arg
								130			135		140		

Glu	Ser	Gln	Ala	Lys	Ala	Arg	Gly	Ile	Pro	Tyr	Glu	Lys	Lys	Lys	Arg
								145			150		155		160

Lys	Arg	Ala	Pro	Thr	Val	Thr	Ala	Arg	Ile	Asp	Val	Ala	Pro	Ser	
								165			170		175		

Arg	Gln	Ser	Glu	Gly	Gly	Cys	Asn	Asp	Ser	Asp	Pro	Ser	Val		
								180			185		190		

Ala	Glu	Ala	Val	Pro	Pro
				195	

<210> SEQ ID NO 91
<211> LENGTH: 672
<212> TYPE: DNA
<213> ORGANISM: Populus balsamifera subsp. trichocarpa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT 1461298
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 92

<400> SEQUENCE: 91

atggactcaa	catctggagt	agcttctgcg	cccgaccgcga	atagtggaga	accgggttcca	60
------------	------------	------------	-------------	------------	-------------	----

tca	tcggat	cat	ttc	atc	tgccatca	ctgccacaac	aacagcaacc	agagggatca	120
-----	--------	-----	-----	-----	----------	------------	------------	------------	-----

tcaccgccc	ag	cac	ccaa	g	ta	gat	gg	act	180
-----------	----	-----	------	---	----	-----	----	-----	-----

ttacagtact	taa	aga	acc	ca	aa	g	cc	ta	240
------------	-----	-----	-----	----	----	---	----	----	-----

gtgatcgagt	tct	tga	ata	ttt	ggat	caa	ttt	gtt	300
------------	-----	-----	-----	-----	------	-----	-----	-----	-----

tggccttatt	ttt	ggc	accc	ga	accc	cc	ttt	gtt	360
------------	-----	-----	------	----	------	----	-----	-----	-----

tgggttagtc	ttt	gtatcg	ctt	cg	aat	ccg	ttt	gtt	420
------------	-----	--------	-----	----	-----	-----	-----	-----	-----

cggccagaat	cg	aa	cc	ttt	gg	ct	tt	gtt	480
------------	----	----	----	-----	----	----	----	-----	-----

gaagggtcaag	cg	aa	cc	ttt	gg	ct	tt	gtt	540
-------------	----	----	----	-----	----	----	----	-----	-----

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gttgctgttg ctacggtgaa tgtgtcggtg gaggcagctg gtggggcgc tactagtggt	600
ggcgaggggg ggagtggta tgctgatagt agtgctgctc cagcagctgc tgctgctaca	660
acaaccgtat ag	672

<210> SEQ ID NO 92
<211> LENGTH: 223
<212> TYPE: PRT
<213> ORGANISM: Populus balsamifera subsp. trichocarpa
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Ceres ANNOT 1461298
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(162)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88

<400> SEQUENCE: 92

Met Asp Ser Thr Ser Gly Val Ala Ser Ala Pro Asp Pro Asn Ser Gly			
1	5	10	15

Glu Pro Gly Pro Ser Ala Gly Ser Ser Ser Ala Ser Ala Ser Leu Pro		
20	25	30

Gln Gln Gln Pro Glu Gly Ser Ser Pro Pro Ala Pro Pro Ser Arg		
35	40	45

Tyr Glu Ser Gln Lys Arg Arg Asp Trp Asn Thr Phe Leu Gln Tyr Leu		
50	55	60

Lys Asn His Lys Pro Pro Leu Thr Leu Ala Arg Cys Ser Gly Ala His			
65	70	75	80

Val Ile Glu Phe Leu Lys Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val		
85	90	95

His Ile Thr Gly Cys Pro Tyr Phe Gly His Pro Asn Pro Pro Ala Pro		
100	105	110

Cys Ser Cys Pro Leu Lys Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile		
115	120	125

Gly Arg Leu Arg Ala Ala Tyr Glu Glu Asn Gly Gly Arg Pro Glu Ser		
130	135	140

Asn Pro Phe Gly Ala Arg Ala Val Arg Ile Tyr Leu Arg Glu Val Arg			
145	150	155	160

Glu Gly Gln Ala Lys Ala Arg Gly Ile Pro Tyr Glu Lys Lys Lys Arg		
165	170	175

Lys Arg Ser Asn Val Ala Val Ala Thr Val Asn Val Ser Val Glu Ala		
180	185	190

Ala Gly Gly Gly Ser Thr Ser Gly Gly Gly Gly Ser Gly Asp Ala		
195	200	205

Asp Ser Ser Ala Ala Ala Ala Ala Ala Ala Thr Thr Thr Val		
210	215	220

<210> SEQ ID NO 93
<211> LENGTH: 212
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa subsp. japonica
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Public GI 34907938
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(145)

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Leu Ser Asn Cys Thr Ser Thr His Val Ile Glu Phe Leu Arg Tyr Leu
 50 55 60
 Asp Pro Phe Gly Lys Thr Lys Val His Thr His Leu Cys Pro Ser Phe
 65 70 75 80
 Gly Gln Pro Asn Pro Pro Thr Leu Cys Pro Cys Pro Leu Arg Gln Ala
 85 90 95
 Trp Gly Ser Leu Asp Ala Leu Ile Gly Arg Leu Arg Ala Ala Phe Glu
 100 105 110
 Glu Asn Gly Gly Gln Pro Glu Ser Asn Pro Phe Gly Ala Arg Ala Val
 115 120 125
 Arg Phe Tyr Leu Arg Glu Val Lys Asp Ala Gln Ala Lys Ala Arg Gly
 130 135 140
 Ile Ser Cys Glu Lys Lys Arg Thr Lys Lys Arg Pro Pro Pro Pro Thr
 145 150 155 160
 Pro Asp Ile Cys Leu Asp Arg
 165

<210> SEQ ID NO 95
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: TUB-F1: Forward primer for tubulin gene amplification

<400> SEQUENCE: 95

gttgagccgt acaatgcaac 20

<210> SEQ ID NO 96
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: TUB-R1: Reverse primer for tubulin gene amplification

<400> SEQUENCE: 96

ctgttcgtcc acttccttg 19

<210> SEQ ID NO 97
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: 05917-F: Forward primer used to detect At1g07090

<400> SEQUENCE: 97

agcaggatcg agtcacagaa gcga 24

<210> SEQ ID NO 98
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: 05917-R: Reverse primer used to detect At1g07090

<400> SEQUENCE: 98

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acagatggag caccgacgtt acaa

24

<210> SEQ ID NO 99
<211> LENGTH: 576
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME16572
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 1285138
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 100

<400> SEQUENCE: 99

atgtcttcgg atcgacac accgacgaaa gatccacccgg atcatccgtc ttcttcctcc	60
aaccaccaca agcaaccact tcctcctcaa ccgcagcaac cactcagccg ctatgaatcg	120
cagaaacgcc gcgactggaa cacgttcgtc caatacaccta aatcacaaaa tccaccgttg	180
atgatgtctc aattcgacta cacgcacgtg ctaagttcc taaggtaactt agatcagttt	240
ggtaagacca aagtacatca tcaagcttgc gtcttcgtc gacaaccggg tccaccagggt	300
cctgtcacgt gtcctctcaa acaagcttgg ggaagcctag atgcttgat cggacggcta	360
agagctgctt acgaggaaca cggtgtgggg tcacctgata ctaaccgtt tgcaaacggg	420
tccatcgaaa ttcaatttgc ggaagtggaa gaatctcaag ccaaggctcg tgggattccg	480
tacaggaaga agaaaaggag gaagactaa aacgaggctcg ttgttgtcaa gaaggatgtt	540
gcacaaactt ctagtccata tcagtagttt acttga	576

<210> SEQ ID NO 100
<211> LENGTH: 188
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME16572
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 1285138
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(152)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 100

Met Ser Ser Asp Arg His Thr Pro Thr Lys Asp Pro Pro Asp His Pro			
1	5	10	15

Ser Ser Ser Asn His His Lys Gln Pro Leu Pro Pro Gln Pro Gln		
20	25	30

Gln Pro Leu Ser Arg Tyr Glu Ser Gln Lys Arg Arg Asp Trp Asn Thr		
35	40	45

Phe Val Gln Tyr Leu Lys Ser Gln Asn Pro Pro Leu Met Met Ser Gln		
50	55	60

Phe Asp Tyr Thr His Val Leu Ser Phe Leu Arg Tyr Leu Asp Gln Phe			
65	70	75	80

Gly Lys Thr Lys Val His His Gln Ala Cys Val Phe Phe Gly Gln Pro		
85	90	95

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Asp Pro Pro Gly Pro Cys Thr Cys Pro Leu Lys Gln Ala Trp Gly Ser
 100 105 110

Leu Asp Ala Leu Ile Gly Arg Leu Arg Ala Ala Tyr Glu Glu His Gly
 115 120 125

Gly Gly Ser Pro Asp Thr Asn Pro Phe Ala Asn Gly Ser Ile Arg Val
 130 135 140

His Leu Arg Glu Val Arg Glu Ser Gln Ala Lys Ala Arg Gly Ile Pro
 145 150 155 160

Tyr Arg Lys Lys Arg Arg Lys Thr Lys Asn Glu Val Val Val Val
 165 170 175

Lys Lys Asp Val Ala Asn Ser Ser Thr Pro Asn Gln
 180 185

<210> SEQ ID NO 101
<211> LENGTH: 573
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME16623
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no.1290753
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME23453
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 853637
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 102

<400> SEQUENCE: 101

atggatttga tctctcacca accaaacaag aaccctaatt cctcaacaca actaacacca	60
ccttcctcaa gccgttacga gaacaaaaaa cgccgtgact ggaacacttt ctgtcaatac	120
ctccggAACCC accgtcttcc gctctcttc ccctcggtta gggcgccaca cgtgctcgag	180
ttccctccgtt accttgacca gttcggaaa acaaaagtcc accaccagaa ctgtgccttc	240
tttggcttcc ctaaccctcc tgctcttgt cttgtcttc tccggcaagc ttggggctca	300
ctcgacgctc ttatcgcccc cctccgcgcc gcctacgagg agaacgggtgg cccacctgaa	360
gctaaccat ttggctcacg cgccgtcagg ttattcctcc gtgaagtca agactttcaa	420
gccaaggctc gaggtgttag ctatgagaag aagaggaaga gagtcaacag gcagaaaccg	480
caaacgcagc cgcctctaca gcttcagcaa cagcaacagc agccacaaca aggtcagtct	540
atgatggcta attactcggt tgcaacagta tga	573

<210> SEQ ID NO 102
<211> LENGTH: 190
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME16623
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 1290753
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME23453
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 853637

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(139)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 102

Met	Asp	Leu	Ile	Ser	His	Gln	Pro	Asn	Lys	Asn	Pro	Asn	Ser	Ser	Thr
1															
														10	15

Gln	Leu	Thr	Pro	Pro	Ser	Ser	Ser	Arg	Tyr	Glu	Asn	Gln	Lys	Arg	Arg	
														20	25	30

Asp	Trp	Asn	Thr	Phe	Cys	Gln	Tyr	Leu	Arg	Asn	His	Arg	Pro	Pro	Leu	
														35	40	45

Ser	Leu	Pro	Ser	Cys	Ser	Gly	Ala	His	Val	Leu	Glu	Phe	Leu	Arg	Tyr	
														50	55	60

Leu	Asp	Gln	Phe	Gly	Lys	Thr	Lys	Val	His	His	Gln	Asn	Cys	Ala	Phe		
														65	70	75	80

Phe	Gly	Leu	Pro	Asn	Pro	Pro	Ala	Pro	Cys	Pro	Cys	Pro	Leu	Arg	Gln	
														85	90	95

Ala	Trp	Gly	Ser	Leu	Asp	Ala	Leu	Ile	Gly	Arg	Leu	Arg	Ala	Ala	Tyr	
														100	105	110

Glu	Glu	Asn	Gly	Gly	Pro	Pro	Glu	Ala	Asn	Pro	Phe	Gly	Ser	Arg	Ala	
														115	120	125

Val	Arg	Leu	Phe	Leu	Arg	Glu	Val	Arg	Asp	Phe	Gln	Ala	Lys	Ala	Arg	
														130	135	140

Gly	Val	Ser	Tyr	Glu	Lys	Lys	Arg	Lys	Arg	Val	Asn	Arg	Gln	Lys	Pro		
														145	150	155	160

Gln	Thr	Gln	Pro	Pro	Leu	Gln	Leu	Gln	Gln	Gln	Gln	Gln	Pro	Gln		
														165	170	175

Gln	Gly	Gln	Ser	Met	Met	Ala	Asn	Tyr	Ser	Gly	Ala	Thr	Val			
														180	185	190

<210> SEQ ID NO 103
<211> LENGTH: 639
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25698
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 1373087
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 104

<400> SEQUENCE: 103

atggatccgt	ctggcccg	tccgtcctct	gcggcggtg	gcggcgcc	ggccgtggc	60
gccccggcc	agccgcggc	gcagctgac	aggtacgagt	cgcagaacgc	gaggactgg	120
aacacgttcc	tgcagtacct	gcggaaccac	cggccggcc	tgacgtggc	gcgggtcagc	180
ggcgcgcacg	tgcgtgggt	cctgaggat	ctggaccat	tcgggaagac	caagggtcac	240
gcgtcggtt	gcgccttcta	cggccagccc	agcccgccgg	ggccgtgccc	gtggccctg	300
cgtcaggcgt	ggggatccct	cgacgcgctc	atcgccgc	tccgcgcgc	gtacgaggag	360
agcggccggca	cgccccggatc	caacccgttc	gccgcgcgc	ccgtccggat	ctacccgcgc	420

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gaggtgcggg actcgaggc caaggcgcc ggcatcccgt acgagaagaa gaagcgcaag	480
cgctcgagg cggegcagcc cgccggcgtc gagccgtccg gctcgcttc tgctgcagct	540
gcagctgccg gtggggaga cgcgggcagc ggtggcggtg cagctgctac taccacagct	600
caacctggag ggagtggcac tgccaccaagc gcctccctga	639

<210> SEQ ID NO 104
<211> LENGTH: 212
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25698
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 1373087
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(145)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 104

Met Asp Pro Ser Gly Pro Gly Pro Ser Ser Ala Ala Ala Gly Gly Ala			
1	5	10	15

Pro Ala Val Ala Ala Ala Pro Gln Pro Pro Ala Gln Leu Ser Arg Tyr		
20	25	30

Glu Ser Gln Lys Arg Arg Asp Trp Asn Thr Phe Leu Gln Tyr Leu Arg		
35	40	45

Asn His Arg Pro Pro Leu Thr Leu Ala Arg Cys Ser Gly Ala His Val		
50	55	60

Ile Glu Phe Leu Arg Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val His			
65	70	75	80

Ala Ser Gly Cys Ala Phe Tyr Gly Gln Pro Ser Pro Pro Gly Pro Cys		
85	90	95

Pro Cys Pro Leu Arg Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile Gly		
100	105	110

Arg Leu Arg Ala Ala Tyr Glu Glu Ser Gly Gly Thr Pro Glu Ser Asn		
115	120	125

Pro Phe Ala Ala Arg Ala Val Arg Ile Tyr Leu Arg Glu Val Arg Asp		
130	135	140

Ser Gln Ala Lys Ala Arg Gly Ile Pro Tyr Glu Lys Lys Lys Arg Lys			
145	150	155	160

Arg Ser Gln Ala Ala Gln Pro Ala Gly Val Glu Pro Ser Gly Ser Ser		
165	170	175

Ser Ala Ala Ala Ala Ala Gly Gly Asp Ala Gly Ser Gly Gly		
180	185	190

Gly Ala Ala Ala Thr Thr Ala Gln Pro Gly Gly Ser Gly Thr Ala		
195	200	205

Pro Ser Ala Ser	
210	

<210> SEQ ID NO 105
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Populus balsamifera subsp. trichocarpa
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25953
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 1440417
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 106

<400> SEQUENCE: 105

atggactcg	catctggagg	agccactgca	ccggccccga	atagtggaga	actttgtcca	60
tca	g	c	a	g	g	
tcagcagcaa	cagcaggatc	gtttagc	tcgcagccac	aacagcaacc	ggagggatca	120
tcaccggcc	caccaccaag	tagatacag	tcacagaaga	ggagagactg	gaacacttc	180
ttacagtaca	taaagaacca	caagccacct	ttaaccctag	ctcggtgcag	tggtgcacat	240
gtgattgagt	tcttgaata	cttggatcaa	tttggtaaga	ctaaagtcca	cataacgggt	300
tgtccttatt	ttgggcaccc	gaacccgcca	gcaccttgtt	cttgtccact	aaagcaggct	360
tggggtagtc	ttgatgcgt	aatcgacgg	cttagagctg	cttatgaaga	aaacgggtga	420
ctgccagaat	caaaccctt	tggggctaga	gctgttagga	tttatttgag	ggaagttcga	480
gaagggtcaag	otaaagccag	aggattcct	tatgagaaga	agaagaagcg	aaaaaggcct	540
aatgttgctg	tttccgtage	gagttgtcg	gtgaaggcag	ctgctggtgg	ctctaata	600
ggcgggtggag	aagaaaatgg	tggtggtgt	gatagtagtg	ccgcccgtac	aagtgtgt	660
goggctgctg	ctacaactac	cgtata	g	g	g	687

<210> SEQ ID NO 106
<211> LENGTH: 228
<212> TYPE: PRT
<213> ORGANISM: Populus balsamifera subsp. trichocarpa
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25953
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 1440417
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(162)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 106

Met	Asp	Ser	Thr	Ser	Gly	Gly	Ala	Thr	Ala	Pro	Gly	Pro	Asn	Ser	Gly
1					5			10					15		

Glu	Pro	Cys	Pro	Ser	Ala	Ala	Thr	Ala	Gly	Ser	Ser	Ser	Ala	Ser	Gln
					20			25					30		

Pro	Gln	Gln	Gln	Pro	Glu	Gly	Ser	Ser	Pro	Pro	Ala	Pro	Pro	Ser	Arg
					35			40			45				

Tyr	Glu	Ser	Gln	Lys	Arg	Arg	Asp	Trp	Asn	Thr	Phe	Leu	Gln	Tyr	Ile
					50			55			60				

Lys	Asn	His	Lys	Pro	Pro	Leu	Thr	Leu	Ala	Arg	Cys	Ser	Gly	Ala	His
					65			70		75			80		

Val	Ile	Glu	Phe	Leu	Lys	Tyr	Leu	Asp	Gln	Phe	Gly	Lys	Thr	Lys	Val
					85			90		95					

His	Ile	Thr	Gly	Cys	Pro	Tyr	Phe	Gly	His	Pro	Asn	Pro	Pro	Ala	Pro
					100			105			110				

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Cys	Ser	Cys	Pro	Leu	Lys	Gln	Ala	Trp	Gly	Ser	Leu	Asp	Ala	Leu	Ile
115				120						125					
Gly	Arg	Leu	Arg	Ala	Ala	Tyr	Glu	Glu	Asn	Gly	Gly	Leu	Pro	Glu	Ser
130				135					140						
Asn	Pro	Phe	Gly	Ala	Arg	Ala	Val	Arg	Ile	Tyr	Leu	Arg	Glu	Val	Arg
145				150					155				160		
Glu	Gly	Gln	Ala	Lys	Ala	Arg	Gly	Ile	Pro	Tyr	Glu	Lys	Lys	Lys	Lys
165				170				175							
Arg	Lys	Arg	Pro	Asn	Val	Ala	Val	Ser	Val	Ala	Ser	Val	Val	Ser	Lys
180					185				190						
Ala	Ala	Ala	Gly	Gly	Ser	Asn	Ser	Gly	Gly	Gly	Glu	Ser	Gly	Gly	
195				200					205						
Gly	Gly	Asp	Ser	Ser	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Ala	Ala	Ala	Ala
210				215					220						
Thr	Thr	Thr	Val												
225															

<210> SEQ ID NO 107
 <211> LENGTH: 723
 <212> TYPE: DNA
 <213> ORGANISM: Populus balsamifera subsp. trichocarpa
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Ceres SEED LINE ME25957
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Ceres ANNOT ID no. 1505805
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 108

<400> SEQUENCE: 107
 atgaattcaa tccaaagaaaat ggagagctcc aactctgaaa acacaaggttt caacagcata 60
 ggcaacagca acaccaccaa cacagccatg tcagtctcaa acttgccacc accatccccc 120
 accactccga gtcgctatga gaatcaaaag cgccgagact ggaacacacctt tggccagttac 180
 ctcaagaacc acaggcctcc tctttctctg tccaggtgca gtgggtctca tgtccttgaa 240
 ttccctcgct accttgacca atttggcaag accaaagtgc acactccaat ctgccccctt 300
 tatggccacc caaacccacc cgccccctgc ccatgccctc tccgcccaggc ctggggtagc 360
 cttgaegcgc tcattggacg cctccgagca gcctttgagg aaaatggagg gaaacctgaa 420
 gcaaaccctt ttggagctcg tgctgtttagg ctgttatctc gtgagggtcg tgattgcag 480
 tctaaagcaa gagggattag ctatgagaaa aagaagcgta agcgtccacc acagcaacaa 540
 atccaaagccc tgccactgcc acttccactg ccaatgccac caccaccaggc tagatctgcg 600
 gataccatga atctgctttt gatgcaaaca gtggtagtaa tattactagt aatggacta 660
 gcggtagtgt tatggctctgt gttgggactg agagcatcta taattgtct tacatttg 720
 taa 723

<210> SEQ ID NO 108
 <211> LENGTH: 240
 <212> TYPE: PRT
 <213> ORGANISM: Populus balsamifera subsp. trichocarpa
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Ceres SEED LINE ME25957
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Ceres ANNOT ID no. 1505805
 <220> FEATURE:

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<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (27)..(159)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 108

Met	Asn	Ser	Ile	Gln	Glu	Met	Glu	Ser	Ser	Asn	Ser	Glu	Asn	Thr	Ser
1						5			10					15	

Phe	Asn	Ser	Ile	Gly	Asn	Ser	Asn	Thr	Thr	Asn	Thr	Ala	Met	Ser	Val
20						25								30	

Ser	Asn	Leu	Pro	Pro	Pro	Ser	Ser	Thr	Thr	Pro	Ser	Arg	Tyr	Glu	Asn
35						40						45			

Gln	Lys	Arg	Arg	Asp	Trp	Asn	Thr	Phe	Gly	Gln	Tyr	Leu	Lys	Asn	His
50						55					60				

Arg	Pro	Pro	Leu	Ser	Leu	Ser	Arg	Cys	Ser	Gly	Ala	His	Val	Leu	Glu
65						70					75			80	

Phe	Leu	Arg	Tyr	Leu	Asp	Gln	Phe	Gly	Lys	Thr	Val	His	Thr	Pro
85						90					95			

Ile	Cys	Pro	Phe	Tyr	Gly	His	Pro	Asn	Pro	Pro	Ala	Pro	Cys	Pro	Cys
100						105					110				

Pro	Leu	Arg	Gln	Ala	Trp	Gly	Ser	Leu	Asp	Ala	Leu	Ile	Gly	Arg	Leu
115						120					125				

Arg	Ala	Ala	Phe	Glu	Glu	Asn	Gly	Gly	Lys	Pro	Glu	Ala	Asn	Pro	Phe
130						135					140				

Gly	Ala	Arg	Ala	Val	Arg	Leu	Tyr	Leu	Arg	Glu	Val	Arg	Asp	Leu	Gln
145						150					155			160	

Ser	Lys	Ala	Arg	Gly	Ile	Ser	Tyr	Glu	Lys	Lys	Lys	Arg	Lys	Arg	Pro
165						170					175				

Pro	Gln	Gln	Ile	Gln	Ala	Leu	Pro	Leu	Pro	Leu	Pro	Met		
180						185					190			

Pro	Pro	Pro	Ala	Arg	Ser	Ala	Asp	Thr	Met	Asn	Leu	Leu	Leu	Met
195						200					205			

Gln	Thr	Val	Val	Val	Ile	Leu	Leu	Val	Met	Gly	Leu	Ala	Val	Val	Leu
210						215					220				

Trp	Ser	Val	Leu	Gly	Leu	Arg	Ala	Ser	Ile	Ile	Ala	Leu	Thr	Phe	Val
225						230					235			240	

<210> SEQ ID NO 109
<211> LENGTH: 660
<212> TYPE: DNA
<223> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25288
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 828846
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 110

<400> SEQUENCE: 109

atggatatga ttccccatt gatgaaaggc tcttcagctt acggagggtgt cacaacactc 60

aacatcatct caaacaactc ctccctcgtc accggagcca ccggagggtga agcaacgcaa 120

ccactgtctt ctcctccctc accatcgccg aactcaagcc gttacgagaa ccagaagagg 180

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agagactgga acacgttcgg acagtactta aggaaccatc ggccaccgct ttgcgttcc	240
cgatgcagtg gagctcacgt gctcgagttc ctccgttact tggaccaggc cggtaaagaca	300
aaagtccaca cgaacatttg tcacttctat ggccatctta atccctccggc accgtgtccg	360
tgtcctctcc gacaagctt gggaaagtctt gacgcttta tcggtegtct tcgagctgcc	420
tttgaggaaa acggaggcaa gcctgagacg aatccctttt gagctcgatgc cgtaggctt	480
tatctaaggg aagtttagaga tatgcagagt aaagctagag gtgttagcta cgagaagaag	540
aagcgaaagc gtcctcttcc ttgcgtcgatc acttcttctt cctccgcccgt agctagccac	600
cagcaatttcaaatgctacc gggtaactgt tctactactc aattaaagtt tgagaagtaa	660

<210> SEQ ID NO 110
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25288
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 828846
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(168)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 110

Met Asp Met Ile Pro Gln Leu Met Glu Gly Ser Ser Ala Tyr Gly Gly			
1	5	10	15

Val Thr Asn Leu Asn Ile Ile Ser Asn Asn Ser Ser Ser Val Thr Gly			
20	25	30	

Ala Thr Gly Glu Ala Thr Gln Pro Leu Ser Ser Ser Ser Ser Pro			
35	40	45	

Ser Ala Asn Ser Ser Arg Tyr Glu Asn Gln Lys Arg Arg Asp Trp Asn			
50	55	60	

Thr Phe Gly Gln Tyr Leu Arg Asn His Arg Pro Pro Leu Ser Leu Ser			
65	70	75	80

Arg Cys Ser Gly Ala His Val Leu Glu Phe Leu Arg Tyr Leu Asp Gln			
85	90	95	

Phe Gly Lys Thr Lys Val His Thr Asn Ile Cys His Phe Tyr Gly His			
100	105	110	

Pro Asn Pro Pro Ala Pro Cys Pro Cys Pro Leu Arg Gln Ala Trp Gly			
115	120	125	

Ser Leu Asp Ala Leu Ile Gly Arg Leu Arg Ala Ala Phe Glu Glu Asn			
130	135	140	

Gly Gly Lys Pro Glu Thr Asn Pro Phe Gly Ala Arg Ala Val Arg Leu			
145	150	155	160

Tyr Leu Arg Glu Val Arg Asp Met Gln Ser Lys Ala Arg Gly Val Ser			
165	170	175	

Tyr Glu Lys Lys Arg Lys Arg Pro Leu Pro Ser Ser Thr Ser			
180	185	190	

Ser Ser Ser Ala Val Ala Ser His Gln Gln Phe Gln Met Leu Pro Gly			
195	200	205	

Thr Ser Ser Thr Thr Gln Leu Lys Phe Glu Lys

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210 215

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<210> SEQ ID NO 111
<211> LENGTH: 495
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME23423
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 832857
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 112

<400> SEQUENCE: 111

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atgacgagta caaacacgag aaacaaaggc aaatgcata tagaaggacc accaccgact      60
ctaaggccgtt atgagtccaca aaaaagccgc gactggaaca cgtttgcca gatatctatg    120
accaagatgc caccaggcata cgtatggag tgtgaatcaa accacatcct cgatttcctc    180
caaagtgcgtg accagtttg taaaacaaaa gttcatatcc aaggatgcgt tttttcgga    240
cagaaagagc caccaggaga gtgtaactgc ccgttgaaac aggccgtgggg aagcttagat   300
gttttgatcg gacggctgag agcagcttac gaggagaacg gtggcttaac ggagaaaaac   360
ccgtttgccc ggggagggat taggatttt ctgagggaa tgagaggttc acaggcgaag   420
gagagaggag tttgtacaa aaaaagaag cgtcttgttag ttgttggtac gggactagt   480
actacttggaa cttaa                                         495

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<210> SEQ ID NO 112
<211> LENGTH: 164
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME23423
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 832857
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(137)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 112

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Met Thr Ser Thr Asn Thr Arg Asn Lys Gly Lys Cys Ile Val Glu Gly
1           5          10          15

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Pro Pro Pro Thr Leu Ser Arg Tyr Glu Ser Gln Lys Ser Arg Asp Trp
20          25          30

```

```

Asn Thr Phe Cys Gln Tyr Leu Met Thr Lys Met Pro Pro Val His Val
35          40          45

```

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Trp Glu Cys Glu Ser Asn His Ile Leu Asp Phe Leu Gln Ser Arg Asp
50          55          60

```

```

Gln Phe Gly Lys Thr Lys Val His Ile Gln Gly Cys Val Phe Phe Gly
65          70          75          80

```

```

Gln Lys Glu Pro Pro Gly Glu Cys Asn Cys Pro Leu Lys Gln Ala Trp
85          90          95

```

```

Gly Ser Leu Asp Ala Leu Ile Gly Arg Leu Arg Ala Ala Tyr Glu Glu

```

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190

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100

105

110

Asn Gly Gly Leu Thr Glu Lys Asn Pro Phe Ala Arg Gly Gly Ile Arg
115 120 125

Ile Phe Leu Arg Glu Val Arg Gly Ser Gln Ala Lys Ala Arg Gly Val
130 135 140

Leu Tyr Lys Lys Lys Arg Leu Val Val Val Gly Thr Gly Thr Ser
145 150 155 160

Thr Thr Trp Thr

<210> SEQ ID NO 113
<211> LENGTH: 576
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME23459
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 847799
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 114

<400> SEQUENCE: 113

atgtcttcgg	atcgacac	accgacgaaa	gatccaccgg	atcatccgtc	ttcttcctcc	60
aaccaccaca	agcaaccact	tcctcccaa	ccgcagcaac	cactcagccg	ctatgaatcg	120
cagaaacgccc	gcgactggaa	cacgttcgct	caatacaccta	aatcacaaaaa	tccaccgtt	180
atgatgtctc	aattcgacta	cacgcacgtg	ctaagttcc	taaggactt	agatcagttt	240
ggtaagacca	aagtacatca	tcaagcttgt	gtcttctcg	gacaaccgga	tccaccaggt	300
ccgtgcacgt	gtcctctcaa	acaagcttg	ggaagcctag	atgcctttag	cgacggcta	360
agagctgctt	acgaggaaca	cggggcggg	tcacctgata	ctaaccgtt	tgcaaacggg	420
tcgatccggg	ttcacttgag	ggaagtgaga	aatctcaag	ccaaggctcg	tgggattccg	480
tacaggaaga	agaaaaggag	gaagactaaa	aacgaggctcg	ttgttgtcaa	gaaggatgtt	540
gcaaaactctt	cgactcctaa	tcagtcgttc	acttga			576

<210> SEQ ID NO 114
<211> LENGTH: 191
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME23459
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 847799
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(152)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 114

Met Ser Ser Asp Arg His Thr Pro Thr Lys Asp Pro Pro Asp His Pro
1 5 10 15

Ser Ser Ser Asn His His Lys Gln Pro Leu Pro Pro Gln Pro Gln
20 25 30

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Gln	Pro	Leu	Ser	Arg	Tyr	Glu	Ser	Gln	Lys	Arg	Arg	Asp	Trp	Asn	Thr
35						40			45						
Phe	Val	Gln	Tyr	Leu	Lys	Ser	Gln	Asn	Pro	Pro	Leu	Met	Met	Ser	Gln
50						55					60				
Phe	Asp	Tyr	Thr	His	Val	Leu	Ser	Phe	Leu	Arg	Tyr	Leu	Asp	Gln	Phe
65						70			75				80		
Gly	Lys	Thr	Lys	Val	His	His	Gln	Ala	Cys	Val	Phe	Phe	Gly	Gln	Pro
									85		90		95		
Asp	Pro	Pro	Gly	Pro	Cys	Thr	Cys	Pro	Leu	Lys	Gln	Ala	Trp	Gly	Ser
									100		105		110		
Leu	Asp	Ala	Leu	Ile	Gly	Arg	Leu	Arg	Ala	Ala	Tyr	Glu	Glu	His	Gly
						115			120			125			
Gly	Gly	Ser	Pro	Asp	Thr	Asn	Pro	Phe	Ala	Asn	Gly	Ser	Ile	Arg	Val
									130		135		140		
His	Leu	Arg	Glu	Val	Arg	Glu	Ser	Gln	Ala	Lys	Ala	Arg	Gly	Ile	Pro
						145			150		155		160		
Tyr	Arg	Lys	Lys	Arg	Arg	Lys	Thr	Lys	Asn	Glu	Val	Val	Val	Val	
						165			170			175			
Lys	Lys	Asp	Val	Ala	Asn	Ser	Ser	Thr	Pro	Asn	Gln	Ser	Phe	Thr	
						180			185			190			

<210> SEQ ID NO 115
<211> LENGTH: 549
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME23517
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 856813
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 116

<400> SEQUENCE: 115

atggaggagg	aaaccgcagc	caaaggcagcg	gcaaggttcct	cctcatcccc	gagccggtag	60
gagtctcaaa	agaggcgaga	ctggaacact	ttccttcagt	atctaaggaa	ccacaaggca	120
cctctgaatc	tgtctcggtt	tagtggcgca	cacgtccttg	agttccttaa	gtacctcgac	180
cagtttggta	agaccaaagt	ccatgccacg	gcttgcctt	tcttcggaca	acctaacc	240
ccgtctcagt	gcacttgc	tctcaagca	gcttggggaa	gtctcgatgc	tctcatccg	300
cgtctaaagg	ctgctttcga	ggaaatcg	ggtggcttc	ctgagtcaaa	cccttcg	360
gccaaggctg	ttaggatcta	tcttaagaa	gtccgtcaaa	cacaggctaa	ggctcgaggg	420
atcccttacg	acaagaagaa	aagaaaacgt	ccgcatacag	acacggcaac	tccaatcg	480
ggtgacggag	acgatgccga	aggaagtgg	ggtgctgctt	tggtcgttac	ggctgcaact	540
acggtatag						549

<210> SEQ ID NO 116
<211> LENGTH: 182
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME23517
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 856813
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(134)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 116

Met	Glu	Gly	Glu	Thr	Ala	Ala	Lys	Ala	Ala	Ala	Ser	Ser	Ser	Ser	Ser
1					5			10						15	

Pro	Ser	Arg	Tyr	Glu	Ser	Gln	Lys	Arg	Arg	Asp	Trp	Asn	Thr	Phe	Leu
			20			25					30				

Gln	Tyr	Leu	Arg	Asn	His	Lys	Pro	Pro	Leu	Asn	Leu	Ser	Arg	Cys	Ser
					35		40				45				

Gly	Ala	His	Val	Leu	Glu	Phe	Leu	Lys	Tyr	Leu	Asp	Gln	Phe	Gly	Lys
	50				55				60						

Thr	Lys	Val	His	Ala	Thr	Ala	Cys	Pro	Phe	Phe	Gly	Gln	Pro	Asn	Pro
65					70			75				80			

Pro	Ser	Gln	Cys	Thr	Cys	Pro	Leu	Lys	Gln	Ala	Trp	Gly	Ser	Leu	Asp
		85				90					95				

Ala	Leu	Ile	Gly	Arg	Leu	Arg	Ala	Ala	Phe	Glu	Glu	Ile	Gly	Gly	Gly
		100			105						110				

Leu	Pro	Glu	Ser	Asn	Pro	Phe	Ala	Ala	Lys	Ala	Val	Arg	Ile	Tyr	Leu
	115					120					125				

Lys	Glu	Val	Arg	Gln	Thr	Gln	Ala	Lys	Ala	Arg	Gly	Ile	Pro	Tyr	Asp
	130					135					140				

Lys	Lys	Lys	Arg	Lys	Arg	Pro	His	Thr	Asp	Thr	Ala	Thr	Pro	Ile	Ala
145					150			155			160				

Gly	Asp	Gly	Asp	Asp	Ala	Glu	Gly	Ser	Gly	Gly	Ala	Ala	Leu	Val	Val
	165					170					175				

Thr	Ala	Ala	Thr	Thr	Val										
				180											

<210> SEQ ID NO 117
<211> LENGTH: 588
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME16579
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 870022
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 118

<400> SEQUENCE: 117

atggctagtc	atacgaaacaa	aggcaaaaggc	atagcagaag	gatcgctc	accgcaatcg	60
caaccgcaac	cacaaccaca	ccaaaccgaa	tcacctccta	acccgc	ccaggc	120
tacgagtac	agaaaacgac	agactggAAC	acgttttgc	aatacctgc	taaccaacag	180
ccaccgggttc	acatctcgca	gtgtggatca	aaccacatcc	tgcattcc	ccaatatctc	240
gaccagtttg	ggaagacaaa	ggttcatatc	catggatgc	tttttttgc	acaggttgag	300
ccagcgggac	agtgttaactg	tcctttaaaa	caagcgtgg	ggagttttaga	tgctttgatc	360
ggacggctaa	gagcggcttt	cgaggagaac	ggaggattgc	cgagagaaaa	cccttttgcc	420
ggcggcggaa	ttagggttt	tctgagggaa	gtgagagatt	cacaggcga	ggcaagagga	480

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gttccgtaca agaaaagaaa aaagaggaag aagaggaatc ctatgaagag tcatgtatggt	540
gaagatggta ctacggAAC tagtagtagC tccaacttgg cttcttag	588

<210> SEQ ID NO 118
<211> LENGTH: 195
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME16579
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres ANNOT ID no. 870022
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (22)..(154)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 118

Met Ala Ser His Ser Asn Lys Gly Lys Gly Ile Ala Glu Gly Ser Ser			
1	5	10	15

Gln Pro Gln Ser Gln Pro Gln Pro Gln Pro His Gln Pro Gln Ser Pro		
20	25	30

Pro Asn Pro Pro Ala Leu Ser Arg Tyr Glu Ser Gln Lys Arg Arg Asp		
35	40	45

Trp Asn Thr Phe Cys Gln Tyr Leu Arg Asn Gln Gln Pro Pro Val His		
50	55	60

Ile Ser Gln Cys Gly Ser Asn His Ile Leu Asp Phe Leu Gln Tyr Leu			
65	70	75	80

Asp Gln Phe Gly Lys Thr Lys Val His Ile His Gly Cys Val Phe Phe		
85	90	95

Gly Gln Val Glu Pro Ala Gly Gln Cys Asn Cys Pro Leu Lys Gln Ala		
100	105	110

Trp Gly Ser Leu Asp Ala Leu Ile Gly Arg Leu Arg Ala Ala Phe Glu		
115	120	125

Glu Asn Gly Gly Leu Pro Glu Arg Asn Pro Phe Ala Gly Gly Ile		
130	135	140

Arg Val Phe Leu Arg Glu Val Arg Asp Ser Gln Ala Lys Ala Arg Gly			
145	150	155	160

Val Pro Tyr Lys Lys Arg Lys Lys Arg Lys Lys Arg Asn Pro Met Lys		
165	170	175

Ser His Asp Gly Glu Asp Gly Thr Thr Gly Thr Ser Ser Ser Asn		
180	185	190

Leu Ala Ser	
195	

<210> SEQ ID NO 119
<211> LENGTH: 838
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24513
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24480
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24762
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1025179
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 120

<400> SEQUENCE: 119

acgatagcct ctcatcttct ttttcctct ccatcatctt ctcttatcaa ctttagactc      60
acaaggctcc tctcatcttc accataacgg aaaaaccaaa caaaaaatcc tttagataatc     120
agatcttgat attatggatc atatcatcggt ctttatgggc acaacaaca tgtcacataa     180
cacaaacctt atgatcgctg ccgcagccac taccactacg acctcttcgt cttcctcttc     240
ttcctccggaa ggctcgaaaa ctaaccagct aagcaggatc gagaatcaga agagaagaga     300
ttggaaacct ttccggacagt atctacgcaa tcaccgtcca ccactttctc tctcccggtt     360
cagtgggtct catgttcttg aattccttagt gtacccgtcga caattcggca agactaaagg     420
tcacacacac ctatgtccgt tcttcggaca cccaaacccca ccagcaccat gtgcctgtcc     480
actccgacaa gcgtggggta gtctggacgc actcattggc cgtcttagag ctgctttga     540
agagaacagggt ggttccaccag agacgaaccc ttttgggca cgagccgttc gactctacct     600
aagggaagta cgtgactcgc aggctaaagc acgtgggatc agctatgaaa aaaagaagcg     660
caagcgaccc cctccggccac taccacccggc tcagccggcg atttcaagta gccctaatta     720
acattaaagtc atgagaatg ttttcaatg aactacgtt gtttacaaat ttttatcaat     780
gacgaacatg cacgagttct tttaaagtca catgccctt cctaaacttt tatttgcac     838

<210> SEQ ID NO 120
<211> LENGTH: 195
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24513
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24480
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24762
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1025179
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
    at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(162)
<223> OTHER INFORMATION: Pfam Name: DUF640
    Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 120

```

Met Asp His Ile Ile Gly Phe Met Gly Thr Thr Asn Met Ser His Asn
 1 5 10 15

Thr Asn Leu Met Ile Ala Ala Ala Ala Thr Thr Thr Thr Ser Ser
 20 25 30

Ser Ser Ser Ser Ser Gly Gly Ser Gly Thr Asn Gln Leu Ser Arg
 35 40 45

Tyr Glu Asn Gln Lys Arg Arg Asp Trp Asn Thr Phe Gly Gln Tyr Leu
 50 55 60

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Arg Asn His Arg Pro Pro Leu Ser Leu Ser Arg Cys Ser Gly Ala His
65 70 75 80

Val Leu Glu Phe Leu Arg Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val
85 90 95

His Thr His Leu Cys Pro Phe Phe Gly His Pro Asn Pro Pro Ala Pro
100 105 110

Cys Ala Cys Pro Leu Arg Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile
115 120 125

Gly Arg Leu Arg Ala Ala Phe Glu Glu Asn Gly Gly Ser Pro Glu Thr
130 135 140

Asn Pro Phe Gly Ala Arg Ala Val Arg Leu Tyr Leu Arg Glu Val Arg
145 150 155 160

Asp Ser Gln Ala Lys Ala Arg Gly Ile Ser Tyr Glu Lys Lys Lys Arg
165 170 175

Lys Arg Pro Pro Pro Pro Leu Pro Pro Ala Gln Pro Ala Ile Ser Ser
180 185 190

Ser Pro Asn
195

<210> SEQ_ID NO 121
<211> LENGTH: 939
<212> TYPE: DNA
<213> ORGANISM: Brassica napus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25665
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1084747
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ_ID NO. 122

<400> SEQUENCE: 121

acactctttc tctcatttc tctctctttt aaaacactaa tcactaaaat cttgattcac 60
tgtatcctca aaaccaactc taaatcaaac tctctcaaag aaaacaagcc aaaggccctac 120
tttggatgga ttcatgggtca caacgaccgg ggcctgtcag cgaaggcgat ccgggtccgt 180
ccatcgtaac cccctttca ccgectgegg cgccctagcag gtacgagtca cagaaacgac 240
gtgactggac cacgttctta cagtagctca agaaccacaa gccgccttt tccttgta 300
ggtagtggcg ggcacatgcc atcgagttcc tcaagtagttt agatcgttc ggttagacca 360
aagtccacgt ggccggcgtgt cttacttcg gccatcagca acctccgtct cttgcgttt 420
gtcctctcaa gcaaggctgg gggctctcg atgcccgtat cggacggctg agagcagcct 480
atggggaa cgggtggacgg cccgagtcga acccggtcgc ggcacgtgcg gtcaggattt 540
acttgaggaa agtcagagaa agtcaagcca aggcccgtgg gagaccctac gagaaaaaga 600
aacggaaacg gccaacaact gttaccacgg tgagagttga cgttgcctccg tcgagacaaa 660
gtgaaggaga tgggtgtAAC atcggtgatc cgtcgctctt ggccgaggct gtacccctt 720
aattacgtta ttattattgt catgatataat taaatacatt atacatgtct ggaactcaca 780
tcaccaaaaa aaaactcaca tcacccctt gagttacta tcgaaaatat atttttggc 840
tagttcagtt gatctttgat gaattacgtt cttgaatttt tcttttaatt ctatgaatt 900
ccacacattt ttaaggacta attaacgagg ttttcattc 939

<210> SEQ_ID NO 122

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<211> LENGTH: 198
<212> TYPE: PRT
<213> ORGANISM: Brassica napus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25665
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1084747
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
    at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(146)
<223> OTHER INFORMATION: Pfam Name: DUF640
    Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 122

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Met Asp Ser Gly Ser Gln Arg Pro Gly Pro Val Ser Glu Gly Asp Pro
 1 5 10 15

Gly Pro Ser Ile Val Thr Pro Ser Ser Pro Pro Ala Ala Pro Ser Arg
 20 25 30

Tyr Glu Ser Gln Lys Arg Arg Asp Trp Thr Thr Phe Leu Gln Tyr Leu
 35 40 45

Lys Asn His Lys Pro Pro Leu Ser Leu Ser Arg Cys Ser Gly Ala His
 50 55 60

Ala Ile Glu Phe Leu Lys Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val
 65 70 75 80

His Val Ala Ala Cys Pro Tyr Phe Gly His Gln Gln Pro Pro Ser Pro
 85 90 95

Cys Ala Cys Pro Leu Lys Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile
 100 105 110

Gly Arg Leu Arg Ala Ala Tyr Glu Glu Asn Gly Gly Arg Pro Glu Ser
 115 120 125

Asn Pro Phe Ala Ala Arg Ala Val Arg Ile Tyr Leu Arg Glu Val Arg
 130 135 140

Glu Ser Gln Ala Lys Ala Arg Gly Arg Pro Tyr Glu Lys Lys Arg
 145 150 155 160

Lys Arg Pro Thr Thr Val Thr Val Arg Val Asp Val Ala Pro Ser
 165 170 175

Arg Gln Ser Glu Gly Asp Gly Cys Asn Ile Gly Asp Pro Ser Ser Leu
 180 185 190

Ala Glu Ala Val Pro Pro
 195

```

<210> SEQ ID NO 123
<211> LENGTH: 802
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25661
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1464359
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 124

<400> SEQUENCE: 123

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agacacacgca cccacacaca cacacacaga gattcacaag caaatcaag aaccctaaaa 60

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tctaaaagaac gtcctgacat aatcacacga tcaaaaaatgg agggagaaac cgcaagtgaag	120
gcagcggcaa gttccctcatc atcacaaccg cgctatgagt cgcaaaagag acgagactgg	180
aacacttcc tacagtatct aaaaaaccac aagccaccc ttacccctgtc tcgttgca	240
ggcgcacacg tcatacgagg ccttaagtac ctgcaccagg ttggtaagac caaagtccac	300
gtcgccggctt gtcccttctt cggagttaccg taccacccgg ttcaagtgcac ttgcctctc	360
aggcaggctt gggggagcct cgactcttc atcggccgtc taagggctgc gttcgaggaa	420
atcgccgggtg gtcttccaga gtcaaaccct ttagctgcca aagcgattag gatctatctt	480
aaagaagttac gtgaaactca ggctaaggct cgagggattc catacgacaa gaagaaacgg	540
aaacgaccc tcatacgctaa ggaaactcag aagcccgtatg atggagaagg tgccgggttga	600
agtggaaagtgt gtgattctgc tttggattt tctgcaactg tggtatagtc caaatataag	660
atgctaaaac taaatataag aaaactttgg catagtaatt ctctccgtgt tctttacttt	720
ataaaatttta tatgttgtgt agtcgtttat ttgagttgtaa gaatgcaatt ataaatggaa	780
aagacggatc atagattatt at	802

<210> SEQ_ID NO 124
<211> LENGTH: 183
<212> TYPE: PRT
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25661
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1464359
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ_ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(134)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 124

Met Glu Gly Glu Thr Ala Val Lys Ala Ala Ala Ser Ser Ser Ser			
1	5	10	15

Pro Ser Arg Tyr Glu Ser Gln Lys Arg Arg Asp Trp Asn Thr Phe Leu			
20	25	30	

Gln Tyr Leu Lys Asn His Lys Pro Pro Leu Thr Leu Ser Arg Cys Ser			
35	40	45	

Gly Ala His Val Ile Glu Phe Leu Lys Tyr Leu Asp Gln Phe Gly Lys			
50	55	60	

Thr Lys Val His Val Ala Ala Cys Pro Phe Phe Gly Val Pro Tyr Pro			
65	70	75	80

Pro Ala Gln Cys Thr Cys Pro Leu Arg Gln Ala Trp Gly Ser Leu Asp			
85	90	95	

Ser Leu Ile Gly Arg Leu Arg Ala Ala Phe Glu Glu Ile Gly Gly			
100	105	110	

Leu Pro Glu Ser Asn Pro Leu Ala Ala Lys Ala Ile Arg Ile Tyr Leu			
115	120	125	

Lys Glu Val Arg Glu Thr Gln Ala Lys Ala Arg Gly Ile Pro Tyr Asp			
130	135	140	

Lys Lys Lys Arg Lys Arg Pro Arg Thr Ala Lys Glu Thr Gln Lys Pro			
145	150	155	160

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Asp Asp Gly Glu Gly Ala Gly Ser Gly Ser Gly Asp Ser Ala Leu
165 170 175

Val Ile Ser Ala Thr Val Val
180

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<210> SEQ ID NO 125
<211> LENGTH: 858
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24758
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25680
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24978
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 604111
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 126
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<400> SEQUENCE: 125

agtcccataa acctcaacttc	ctcaaacctca	atccaacaga	aacaaaaaaaaa	aacctcaactt	60
agatcacata gatcaaacaa	caaaaacacag	agttaccta	attgaacctta	ccccagtagg	120
ttctacaagg tcttgatcat	ggcctcagca	tca	aggggagg	caccaccacc	180
tcaacagaag ctgctccage	atcaggctct	tca	gtcc	ccatatcagc	240
caacccggag gatcatcgcc	ggcgctccg	agccgctacg	aatcgaaaaa	gcgtcgagac	300
tggAACACGT ttctgcagta	cctgcagaac	caca	ggccc	cattaacgct	360
agtggcgac acgtcattga	gttcttgaag	tacttggacc	aattcggaa	aaccaagg	420
cacatcacgg ggtgcccgta	ctacgggtac	ccc	aaaccctc	ctgcgc	480
ctgaaacaag cgtggggaaag	ccttgacgccc	ctgatcggc	gactcagg	ggcttacgag	540
aaaaacggag gccgcctga	gtctaacc	ttcggc	ggccgtc	aatttac	600
agggaggtaa gagaaggta	ggctaaagca	agagg	gtcc	ttatgagaa	660
aaggaggaca ccgtggtgac	ggtgagt	ggtggtgg	gtat	gagg	720
tctccgagtg gcgggtgtga	taccgctatt	ggtggtgg	ctgg	ttctag	780
acttcttcag caactgccac	agcta	atgtat	actaca	acc	840
tttaattatt tattttc					858

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<210> SEQ ID NO 126
<211> LENGTH: 229
<212> TYPE: PRT
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24758
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25680
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24978
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 604111
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
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at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (28)...(107)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 126

Met Ala Ser Ala Ser Gly Glu Ala Pro Pro Pro Gln Pro Thr Ser Thr			
1	5	10	15
Glu Ala Ala Pro Ala Ser Gly Ser Ser Ala Pro Ala Ile Ser Ala Ala			
20	25	30	
Pro Pro Gln Pro Gly Gly Ser Ser Pro Ala Pro Pro Ser Arg Tyr Glu			
35	40	45	
Ser Gln Lys Arg Arg Asp Trp Asn Thr Phe Leu Gln Tyr Leu Gln Asn			
50	55	60	
His Lys Pro Pro Leu Thr Leu Ala Arg Cys Ser Gly Ala His Val Ile			
65	70	75	80
Glu Phe Leu Lys Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val His Ile			
85	90	95	
Thr Gly Cys Pro Tyr Tyr Gly Tyr Pro Asn Pro Pro Ala Pro Cys Ala			
100	105	110	
Cys Pro Leu Lys Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile Gly Arg			
115	120	125	
Leu Arg Ala Ala Tyr Glu Asn Gly Gly Arg Pro Glu Ser Asn Pro			
130	135	140	
Phe Gly Ala Arg Ala Val Arg Ile Tyr Leu Arg Glu Val Arg Glu Gly			
145	150	155	160
Gln Ala Lys Ala Arg Gly Ile Pro Tyr Glu Lys Lys Lys Arg Lys Arg			
165	170	175	
Thr Thr Val Val Thr Val Ser Ser Gly Gly Gly Ser Ser Gly Ala			
180	185	190	
Val Ala Ser Pro Ser Gly Gly Asp Thr Ala Ile Gly Gly Ala			
195	200	205	
Gly Ser Ser Ala Ser Leu Thr Ser Ser Ala Thr Ala Thr Ala Asn Asp			
210	215	220	
Thr Thr Thr Thr Val			
225			

<210> SEQ ID NO 127
<211> LENGTH: 897
<212> TYPE: DNA
<213> ORGANISM: Brassica napus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25647
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 964932
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 128

<400> SEQUENCE: 127

acgataccccc ctcctctcct ccttttct ctccaccatc ttcccttatac aactcaagac	60
ccataaaaggta caagactcaa gactcataaa gtcctctca tattcatcat aacctaaaac	120
caaaaacctca aagagttaat aaaacctaaa ttatacatca gatcttgata tcatggatcc	180
tatccacggc tttatgagca catcaaacat ctcacacaac acaaacctta tgatcgccgc	240

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cgcagcagcc accactacca ctacccctc ctcctcgctc tccctctggcg gctccgcac	300
aaaccaactg agtaggtacg agaatcagaa gagaagagac tggAACACTT tcggacaata	360
tctacgcaac caccgtccac cactttctct ctcccgttgc agtggtgctc atgttcttga	420
gttcctcagg tacctcgacc aattcggcaa gaccaaggtt cacatgcaaa tatgtccctt	480
cttggacac ccaaaccac cagcacatg tacctgccc ctcagacaag cgtggggcag	540
cctcgacgca ctcattggcc ggcttcgagc tgctttgaa gagaacgggtt gttcaccaga	600
gacgaaccct tttggtgcac gagctgttcg actctaccta agggaaagttc gtgattcgca	660
ggcttaaagcg cgtggatca gctatgaaaa gaagaagcgg aagcgaccctc ctcaggcgcc	720
actaccacccg cctcatcagc cggtgatttc gaatagtccct aatttgcaat aagtcatatc	780
agtaagatat gttttagtca actacgttcc ttacaactt tatatagtat ttgtcaatga	840
cgaacatgca ggagttgtct aaaaagctgc atgccctct cttttatttg gccagct	897

<210> SEQ_ID NO 128
<211> LENGTH: 199
<212> TYPE: PRT
<213> ORGANISM: Brassica napus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME25647
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 964932
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ_ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(162)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 128

Met Asp Pro Ile His Gly Phe Met Ser Thr Ser Asn Ile Ser His Asn			
1	5	10	15
Thr Asn Leu Met Ile Ala Ala Ala Ala Thr Thr Thr Thr Ser			
20	25	30	
Ser Ser Ser Ser Ser Gly Gly Ser Ala Thr Asn Gln Leu Ser Arg			
35	40	45	
Tyr Glu Asn Gln Lys Arg Arg Asp Trp Asn Thr Phe Gly Gln Tyr Leu			
50	55	60	
Arg Asn His Arg Pro Pro Leu Ser Leu Ser Arg Cys Ser Gly Ala His			
65	70	75	80
Val Leu Glu Phe Leu Arg Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val			
85	90	95	
His Met Gln Ile Cys Pro Phe Phe Gly His Pro Asn Pro Pro Ala Pro			
100	105	110	
Cys Thr Cys Pro Leu Arg Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile			
115	120	125	
Gly Arg Leu Arg Ala Ala Phe Glu Glu Asn Gly Gly Ser Pro Glu Thr			
130	135	140	
Asn Pro Phe Gly Ala Arg Ala Val Arg Leu Tyr Leu Arg Glu Val Arg			
145	150	155	160
Asp Ser Gln Ala Lys Ala Arg Gly Ile Ser Tyr Glu Lys Lys Lys Arg			
165	170	175	
Lys Arg Pro Pro Gln Ala Pro Leu Pro Pro His Gln Pro Val Ile			

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180

185

190

Ser Asn Ser Pro Asn Leu Gln
195

```
<210> SEQ ID NO 129
<211> LENGTH: 874
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24507
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 604111
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 146

<400> SEQUENCE: 129
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agtcccataa acctcacttc ctcaaccta atccaaacaga aacaaaaaaaaaacctcactt	60
agatcacata gatcaaacaa caaaaacacag agttaccta attgaaccta ccccgtagg	120
ttctacaagg tcttgatcat ggccctcagca tcaggggggg caccaccacc ccaacccact	180
tcaacagaag ctgctccagc atcaggctct tcagctccag ccataatcagc agcaccacca	240
caacccggag gatcatcgcc ggccgcctccg agccgctacg aatcgaaaaa gcgtcgagac	300
tggAACACGT ttctgcagta cctgcagaac cacaagcccc cattaacgct ggccgcgtgc	360
agtggcgac acgtcattga gttcttgaag tacttgacc aattcgaaaa aaccaaggtt	420
cacatcacgg ggtgcccgta ctacgggtac cccaaccctc ctgcgcgcctg cgcttgcaca	480
ctgaaacaag cgtggggaaag ctttgacgccc ctgatcgggc gactcaggc ggcttacgag	540
gaaaacggag gccgcctga gtctaaccccg ttcggcgcca gggccgtcag aatttacctc	600
agggaggtaa gagaaggtca ggctaaagca agagggatcc cttatgagaa gaagaacgg	660
aagaggacca ccgtggtgac ggtgagtagt ggtgggtggt gtagtagcgg tgcaagtggcc	720
tctccgagtg gcgggtgtga taccgctatt ggtggtgag ctggttctag tgctagttt	780
acttcttcag caactgccac agctaattgt actacaacca cagtataatt ttaatagttt	840
tttaattttt tattttcaa aaaaaaaaaaaa aaaa	874

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<210> SEQ ID NO 130
<211> LENGTH: 1278
<212> TYPE: DNA
<213> ORGANISM: Gossypium hirsutum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1855399
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 131
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<400> SEQUENCE: 130	
aaatcttcc cgtgaaagga tccccatggag cactacttct ttcaatgaac cctaaacacc	60
ctcaattatc atactcttat ttgactgacc taatcaaaca gaagcagctt ataagggttt	120
gtcaatttgtg agtgactgtat aaatagctt gatTTGGAA tctctcccta cacttggatt	180
tcaaaaaaaa acaaaaatccc aggtggaaaa aattcatcac tgcccatcaa cagttcatca	240
ccaaaaacccc aacagtttcc tctttttttt ttccaagtca atggattctg cctccggagg	300
gagtgacaat agcatcaaag aggctatacc agcaacagct tcagccctgc tgtccgcggc	360
ttcacaacaa ggaggaggag gtggtagtga gtcgtctcct tccccagctc caccgagtag	420

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gtacgagtca caaaagcgtc gagactggaa cacttcttg cagtaattga ccaaccataa	480
accccccatta acactagctc gttcagtgg cgcacacgtatggatgttct tgaaaataacct	540
tgaccaggatc ggcaagacta aggttcacat aacggattgt ccctatttcg gacatgtaaa	600
cccacctgtc ccctgcgtt gcccaactgaa gcaagcgtgg ggtagectcg acgcgtgtat	660
cggacggctc agagctgctt atgaagaaaa cggtggacgt ccagaatcca accctttgg	720
cgcaagggt gtgaggatatttggatggaa agtgagagaaa gggcaggcta aagctagagg	780
gattccttat gagaagaaga agcgaaaaag gcccaactgtc acaactacgg ctgtcggtt	840
caatgttcc aggacttcca ctcaccagt tggatggcggtt gggggtcggtt gggcattgg	900
tggatggat gatagtgttgc tggctaaac tggggcaaat gttggtagtg ccaccgcagt	960
tgctgtgtctt accactaataa gctgtatagtt cttttccctt attaacaatat tctttcttc	1020
ttttttgcctt ttaaacagct gttttaatgt tgattacgag ttatataatat ctggtggttc	1080
tgtcgaaaaa ttggatttgc atccccatgaa ccaaatttag aatttaggtt gaattcttagt	1140
ttaatctctt ttcaatcaat ctctccattt ttcccccttc totactttct tcatttttc	1200
ttgctatgca tggatgttgc aaaggaatat aagaagttt aatcttttcccttctaa	1260
aaaaaaaaaaaaaaa aaa	1278

<210> SEQ ID NO 131
<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: Gossypium hirsutum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1855399
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (29)..(161)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 131

Met Asp Ser Ala Ser Gly Gly Ser Asp Asn Ser Ile Lys Glu Ala Ile			
1	5	10	15

Pro Ala Thr Ala Ser Ala Leu Leu Ser Ala Ala Ser Gln Gln Gly Gly			
20	25	30	

Gly Gly Gly Ser Glu Ser Ser Pro Ser Pro Ala Pro Pro Ser Arg Tyr			
35	40	45	

Glu Ser Gln Lys Arg Arg Asp Trp Asn Thr Phe Leu Gln Tyr Leu Thr			
50	55	60	

Asn His Lys Pro Pro Leu Thr Leu Ala Arg Cys Ser Gly Ala His Val			
65	70	75	80

Ile Glu Phe Leu Lys Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val His			
85	90	95	

Ile Thr Asp Cys Pro Tyr Phe Gly His Val Asn Pro Pro Ala Pro Cys			
100	105	110	

Ala Cys Pro Leu Lys Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile Gly			
115	120	125	

Arg Leu Arg Ala Ala Tyr Glu Glu Asn Gly Gly Arg Pro Glu Ser Asn			
130	135	140	

Pro Phe Gly Ala Arg Ala Val Arg Ile Tyr Leu Arg Glu Val Val Arg Glu	
---	--

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145	150	155	160
Gly Gln Ala Lys Ala Arg Gly Ile Pro Tyr Glu Lys Lys Lys Arg Lys			
165	170	175	
Arg Pro Thr Val Thr Thr Ala Val Gly Val Asn Val Ser Arg Thr			
180	185	190	
Ser Thr Gln Pro Val Asp Gly Gly Gly Arg Gly Gly Ile Gly Gly			
195	200	205	
Gly Asp Asp Ser Val Gly Ala Lys Thr Gly Ala Asn Val Gly Ser Ala			
210	215	220	
Thr Ala Val Ala Ala Ala Thr Thr Asn Ser Val			
225	230	235	

<210> SEQ ID NO 132
<211> LENGTH: 2276
<212> TYPE: DNA
<213> ORGANISM: *Panicum virgatum*
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1858527
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 133

<400> SEQUENCE: 132

gtccccggcat atctgaccac atcttcttcc cccacacctc cccaaagctcg ctcacccatcg	60
ctgctggcct cctccctctcc cgtecccttcc caccgatcga gtttcttcta actgttgtta	120
tgcgtgccttc gtgttcaact cgagccgtcg ctttgcaatt ctttgcatac ttttttgc当地	180
aaaaaaaaatct ttgttatgcat gtttcatgtt tctgaagctg tacgattgtat ctttgtgtct	240
ttatccggct catcatccgc acatctgtcc atgcatgtcg tcagcttgc ttgtgttagct	300
tctgtttccc tggtgtctgg tgcgcgcgtc gtgcgcgcac ggattgtcta gtggtaggct	360
cgtggccctg cgcctcactg acgecccacac atggatcaag ggccctgtaa accctgtct	420
gcagcgaccc accgtgtcgta tcattaacgg ggccgcgcaca ctctggctgt tctggatcaa	480
tgcgccttcg ctttcttggaa gttagtaggt agacgcatgt tgcacagtgc tctccctct	540
tttctgtatgc acctcgact catctctggc attcaggcag agccgaccag ccagctctg	600
aataaaactga atgtttgtcg acctctagtc ctgcctctgt tgcgtctgtt ttgctcaccg	660
atcgccggcg tggcgccaggc gaagccgaaa tttttctgtt atttgcgtt cagttttgtt	720
ttactcctcc gttccgttttgc tgcgttttgc ccctttcccc tgcgtttgc ttcaagacttt	780
ccgtgttaggc gtcagttctt gcatgtctgc taaggatcag cggccctcagt cctcagggtgc	840
tctagacttg aaatcccact accgggttgcgat aggtactact aggtggccgc tagctccgac	900
ctgaaaccct agttcattca gaatatctga tccgtccttag ctctgtggc cggccaagaa	960
cagacgaagc gactgtttct tgcgttgcgac gcccctttgc atacgtatcgt tattattgtt	1020
tcttgcgcga ccattggcgcgaa aagcgttgcgac tcaacaggca tggcacatgg tgccggcgtca	1080
gggtcagatc tgggttggcc ttgcgtggaca ggctgcggcg aaggagctat ggagatggcc	1140
ggcgccggcga acagcccccggg cccggcagcg ggcggccgcg gccggatcga gtcgcagaag	1200
cgccggggact ggcagacgtt cggggcagtc ctgcgcacacc accggccggcc gctggagctg	1260
gcccgggtcga gcgccgcgcgca cgtgcgtcgag ttccctccgcgat acctggacca gtcggcaag	1320
accaagggtgc acgcgcgcggg gtgcccccttc ttgcggccacc cgtcgccgcg ggcggccgtgc	1380
ccgtgccccgc tcaagcaggc gtggggcagc ctcgcacgcgc tgcgtggccg cctccgcgcc	1440

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gccttcgagg	agcaacggcgg	ccgccccgag	gccaatccct	tcggttgcg	cggcgtccgg	1500
ctcttaccc	gcgagggtccg	cgacacccag	gccaaggcgc	ggggcatcgc	ctacgagaag	1560
aaggcgcgca	agcgcacacc	gccggcacac	aggcaggcga	agcagcagca	ggacgcccgc	1620
cagcagcagc	agcagcagca	ctaccaccc	caccaccacc	accaggcg	gcccgcgcg	1680
gttgtcggt	ccgagagtag	gcgcgtgt	ggggacatgg	ccgagccgt	gggcgcgcac	1740
ttcctgtatcc	cgcaecgc	gttctccac	ggccacttcc	tgggtcggt	caccgagccg	1800
accgaccccg	ccgcgggcat	gggggggggc	ggcacccggc	aggacttggt	gttgcaatg	1860
gccccggccg	ccgaggcgca	cggccgcgcg	gggggttct	tgtgtcggt	gtccgtgtt	1920
cactagctag	cttgcgtgggt	ccactctccg	ctgccttat	agctccagg	gcaggatgc	1980
aaggcttagt	aattaggcgt	aatcaagcat	gcaggtttt	ctaattggca	tcggcctgat	2040
ctctgcgcgc	cgtttggcgt	tccatccggc	ttttgggtgt	tatgcgttg	catcaaccgc	2100
tgctgcctt	tggttgtatt	ttttctccat	gacttggatc	ttgtggaaat	ttcatgtact	2160
gattagacccg	ctgtgtgtgt	ttttctccat	gacttggatc	ttgtggaaat	ttcatgtact	2220
acagctgate	tcaatcgact	taacattgtt	cctggtaaaa	aaaaaaaaaa	aaaaaaa	2276

<210> SEQ_ID NO 133
 <211> LENGTH: 288
 <212> TYPE: PRT
 <213> ORGANISM: Panicum virgatum
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Ceres CLONE ID no. 1858527
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
 at SEQ_ID NO. 88
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (24)..(156)
 <223> OTHER INFORMATION: Pfam Name: DUF640
 Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 133

Met	Ala	His	Gly	Ala	Gly	Ala	Asp	Leu	Gly	Trp	Pro	Ser	Trp
1				5			10			15			

Thr	Gly	Cys	Gly	Glu	Gly	Ala	Met	Glu	Met	Ala	Gly	Ala	Ala	Asn	Ser
						20		25					30		

Pro	Gly	Pro	Ala	Ala	Ala	Arg	Pro	Ser	Arg	Tyr	Glu	Ser	Gln	Lys	Arg
						35		40			45				

Arg	Asp	Trp	Gln	Thr	Phe	Gly	Gln	Tyr	Leu	Arg	Asn	His	Arg	Pro	Pro
						50		55		60					

Leu	Glu	Leu	Ala	Arg	Cys	Ser	Gly	Ala	His	Val	Leu	Glu	Phe	Leu	Arg
						65		70		75		80			

Tyr	Leu	Asp	Gln	Phe	Gly	Lys	Thr	Lys	Val	His	Ala	Pro	Gly	Cys	Pro
						85		90		95					

Phe	Phe	Gly	His	Pro	Ser	Pro	Pro	Ala	Pro	Cys	Pro	Cys	Pro	Leu	Lys
						100		105		110					

Gln	Ala	Trp	Gly	Ser	Leu	Asp	Ala	Leu	Val	Gly	Arg	Leu	Arg	Ala	Ala
						115		120		125					

Phe	Glu	Glu	His	Gly	Gly	Arg	Pro	Glu	Ala	Asn	Pro	Phe	Gly	Val	Arg
						130		135		140					

Ala	Val	Arg	Leu	Tyr	Leu	Arg	Glu	Val	Arg	Asp	Thr	Gln	Ala	Lys	Ala
						145		150		155		160			

Arg	Gly	Ile	Ala	Tyr	Glu	Lys	Lys	Arg	Arg	Lys	Arg	His	Pro	Pro	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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165	170	175
His Arg Gln Ala Lys Gln Gln Gln Asp Ala Gly Gln Gln Gln Gln Gln		
180	185	190
Gln His Tyr His Pro His His His His Gln Ala Ser Pro Ala Ala Ala		
195	200	205
Ala Val Thr Glu Ser Arg Arg Val Leu Ala Asp Met Ala Glu Pro Leu		
210	215	220
Ala Pro His Phe Leu Ile Pro His Ala Gln Phe Leu His Gly His Phe		
225	230	235
Leu Val Pro Val Thr Glu Pro Thr Asp Pro Ala Ala Gly Met Gly Gly		
245	250	255
Gly Gly Thr Gly Glu Asp Leu Val Leu Ala Met Ala Ala Ala Ala Glu		
260	265	270
Ala His Ala Ala Ala Ala Gly Phe Leu Met Pro Leu Ser Val Phe His		
275	280	285

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<210> SEQ ID NO 134
<211> LENGTH: 797
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1896482
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 135
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<400> SEQUENCE: 134

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<210> SEQ ID NO 135
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1896482
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
    at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<222> LOCATION: (28)..(160)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 135

Met	Asp	Ser	Ala	Thr	Asp	Pro	Asn	Thr	Ile	Lys	Glu	Asp	Pro	Val	Ser
1									5	10					15

Val Thr Val Ser Ala Pro Pro Ser Lys Gly Ile Gln Gln Gly Val Gly

20									25	30					
----	--	--	--	--	--	--	--	--	----	----	--	--	--	--	--

Glu Ser Pro Ser Ser Ser Thr Ser Pro Ala Ala Pro Ser Arg Tyr Glu

35									40	45					
----	--	--	--	--	--	--	--	--	----	----	--	--	--	--	--

Ser Gln Lys Arg Arg Asp Trp Asn Thr Phe Leu Gln Tyr Leu Lys Asn

50									55	60					
----	--	--	--	--	--	--	--	--	----	----	--	--	--	--	--

His Lys Pro Pro Leu Thr Leu Ala Arg Cys Ser Gly Ala His Val Ile

65									70	75					80
----	--	--	--	--	--	--	--	--	----	----	--	--	--	--	----

Glu Phe Leu Lys Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val His Met

85									90	95					
----	--	--	--	--	--	--	--	--	----	----	--	--	--	--	--

Thr Gly Cys Pro Tyr Phe Gly His Pro Asn Pro Pro Gly Pro Cys Ser

100									105	110					
-----	--	--	--	--	--	--	--	--	-----	-----	--	--	--	--	--

Cys Pro Leu Lys Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile Gly Arg

115									120	125					
-----	--	--	--	--	--	--	--	--	-----	-----	--	--	--	--	--

Leu Arg Ala Ala Tyr Glu Glu Ser Gly Gly Arg Pro Glu Ser Asn Pro

130									135	140					
-----	--	--	--	--	--	--	--	--	-----	-----	--	--	--	--	--

Phe Ala Ala Arg Ala Val Arg Ile Tyr Leu Arg Glu Val Arg Glu Gly

145									150	155					160
-----	--	--	--	--	--	--	--	--	-----	-----	--	--	--	--	-----

Gln Ala Arg Ala Arg Gly Ile Pro Asn Glu Lys Lys Lys Arg Lys Arg

165									170	175					
-----	--	--	--	--	--	--	--	--	-----	-----	--	--	--	--	--

Thr Ser Val Thr Thr Ser Ala Val Gly Ile Asn Val Ser Ala Val Ala

180									185	190					
-----	--	--	--	--	--	--	--	--	-----	-----	--	--	--	--	--

Ala Thr Gln Ala Val Asp Tyr Gly Gly Val Ser Gly Gly Thr Ala Ser

195									200	205					
-----	--	--	--	--	--	--	--	--	-----	-----	--	--	--	--	--

Asn Leu Gly Thr Ala Thr Thr Thr Ser Leu

210									215						
-----	--	--	--	--	--	--	--	--	-----	--	--	--	--	--	--

<210> SEQ ID NO 136
<211> LENGTH: 1125
<212> TYPE: DNA
<213> ORGANISM: Gossypium hirsutum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1934537
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 137

<400> SEQUENCE: 136

aagaattatt	ttttggacgt	ctcatcattt	agtttttttt	tccctctctt	cacactttat	60
cacttcaaat	ttcttcctcg	ttttgatttt	cattcaaaac	catactctgaa	ttgtttttta	120
aaagccaatc	tgcggatccc	agcagttttt	tcaagtgaacc	ctagtcaaaa	agagaagcag	180
ctagagcaaa	gagtttatga	attgttagtg	attgattgtat	tgtatgtata	tgttagagtt	240
tatataaaaa	agaaaacgac	gatttgatgg	aaatttatgt	acagccaatt	atcatcaaaa	300
gtgcgaagcc	ctaatacgat	tttttaagtc	aatggattct	gcaacgaacc	cgaatatcat	360
caagaaggat	ccatgttcc	ttcacatcg	agcaccatcg	tccacgggta	tccagcaagg	420
agttggtgag	tcgcggcggt	cttctacttc	cccagcagca	ccgagtcggt	acgagtcaca	480
aaagcgctcg	gactggaaaca	cgttcttgc	gtacttgaag	aaccataagc	cggcatttgc	540

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tctggctcg	tgcagcggcg	cacacgtat	cgagttcttg	aagtacacctg	accagttcg	600
gaaaaccaag	gttcacatga	cgggttgc	ttatccggaa	cacccgaaacc	cgcctggcc	660
ttgctttgt	ccactcaagc	aagcgtgggg	tagcctcgac	gctgtatcg	gacggctgag	720
agctgcttac	gaagagagcg	ggggacgacc	gaaatcgaa	ccgtttcg	caagggttgt	780
gaggattat	ttgagggaaag	tgagggaaagg	acaggctaga	gctagaggga	taccttatga	840
aaaaaaaag	cgaaaaaggc	cttctgtcac	aactagcgct	gtaggggtca	atgtgtcg	900
ggggctgcc	actcaagcgg	ttgattatgg	tggggtagc	ggaggaactg	cgggtatct	960
tgttactgt	actaccacta	ctagttata	aattcttcaa	tgattattat	atatatata	1020
atggcttca	atatttgata	taaatgtat	atgtggcggt	tctttcttaa	aattggatcc	1080
atatccccat	gaaccaaatt	tagacaaaaa	aaaaaaaaaa	aaaaaa		1125

<210> SEQ ID NO 137
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Gossypium hirsutum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1934537
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (28)..(160)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 137

Met	Asp	Ser	Ala	Thr	Asn	Pro	Asn	Ile	Ile	Lys	Lys	Asp	Pro	Val	Pro
1								5		10				15	
Val	Thr	Val	Ser	Ala	Pro	Ser	Ser	Thr	Gly	Ile	Gln	Gln	Gly	Val	Gly
		20						25						30	
Glu	Ser	Pro	Ser	Ser	Ser	Thr	Ser	Pro	Ala	Ala	Pro	Ser	Arg	Tyr	Glu
		35					40						45		
Ser	Gln	Lys	Arg	Arg	Asp	Trp	Asn	Thr	Phe	Leu	Gln	Tyr	Leu	Lys	Asn
	50					55			60						
His	Lys	Pro	Pro	Leu	Thr	Leu	Ala	Arg	Cys	Ser	Gly	Ala	His	Val	Ile
	65					70			75				80		
Glu	Phe	Leu	Lys	Tyr	Leu	Asp	Gln	Phe	Gly	Lys	Thr	Lys	Val	His	Met
	85				90			95							
Thr	Gly	Cys	Pro	Tyr	Phe	Gly	His	Pro	Asn	Pro	Pro	Gly	Pro	Cys	Ser
	100				105			110							
Cys	Pro	Leu	Lys	Gln	Ala	Trp	Gly	Ser	Leu	Asp	Ala	Leu	Ile	Gly	Arg
	115				120			125							
Leu	Arg	Ala	Ala	Tyr	Glu	Glu	Ser	Gly	Gly	Arg	Pro	Glu	Ser	Asn	Pro
	130				135			140							
Phe	Ala	Ala	Arg	Ala	Val	Arg	Ile	Tyr	Leu	Arg	Glu	Val	Arg	Glu	Gly
	145				150			155			160				
Gln	Ala	Arg	Ala	Arg	Gly	Ile	Pro	Tyr	Glu	Lys	Lys	Arg	Lys	Arg	
	165				170			175							
Pro	Ser	Val	Thr	Thr	Ser	Ala	Val	Gly	Val	Asn	Val	Ser	Ala	Val	Ala
	180				185			190							
Ala	Thr	Gln	Ala	Val	Asp	Tyr	Gly	Gly	Ser	Gly	Gly	Thr	Ala	Gly	
	195				200			205							

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Asn Leu Gly Thr Ala Thr Thr Thr Ser Leu
210 215

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<210> SEQ ID NO 138
<211> LENGTH: 1159
<212> TYPE: DNA
<213> ORGANISM: Gossypium hirsutum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1942084
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 139
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<210> SEQ ID NO 139
<211> LENGTH: 218
<212> TYPE: PRT
<213> ORGANISM: Gossypium hirsutum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1942084
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
    at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (27)..(159)
<223> OTHER INFORMATION: Pfam Name: DUF640
    Pfam Description: Protein of unknown function (DUF640)
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<400> SEQUENCE: 139

Met Asp Ser Gly Ser Gly Ala Asn Pro Asn Ser Ile Asn Glu Gly Ser

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1	5	10	15
Ser Ser Ala Thr Ala Pro Val Leu Met Asp Ser Gln Gln Gly			Gly Ala
20	25		30
Gly Glu Leu Ser Ser Ser Pro Ala His Pro Pro Ser Arg Tyr Glu Ser			
35	40		45
Gln Lys Arg Arg Asp Trp Asn Thr Phe Leu Gln Tyr Leu Lys Asn His			
50	55		60
Lys Pro Pro Leu Thr Leu Ser Arg Cys Ser Gly Ala His Val Ile Glu			
65	70		80
Phe Leu Lys Tyr Leu Asp Gln Phe Gly Lys Thr Lys Val His Val Thr			
85	90		95
Ala Cys Pro Tyr Phe Gly His Ala Asn Pro Pro Asp Pro Cys Ser Cys			
100	105		110
Pro Leu Lys Gln Ala Trp Gly Ser Leu Asp Ala Leu Ile Gly Arg Leu			
115	120		125
Arg Ala Ala Tyr Glu Glu Asn Gly Gly Arg Arg Glu Ser Asn Pro Phe			
130	135		140
Gly Thr Arg Ala Val Arg Ile Tyr Leu Arg Glu Val Arg Gly Gly Gln			
145	150		155
Ala Lys Ala Arg Gly Ile Pro Tyr Glu Lys Lys Lys Arg Lys Arg Pro			
165	170		175
Thr Thr Thr Ala Val Ser Ala Ala Ser Gly Thr Gln Pro Pro Gly Gly			
180	185		190
Ala Ala Gly Asp Asp Ser Ser Gly Gly Thr Thr Ala Asn Val Gly Thr			
195	200		205
Val Thr Ala Ala Ala Thr Thr Asn Ser Leu			
210	215		

<210> SEQ ID NO 140
<211> LENGTH: 1533
<212> TYPE: DNA
<213> ORGANISM: Panicum virgatum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1988960
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 141

<400> SEQUENCE: 140

acctctcccc aagctcgctc aactcagctg ctggccctcc ttcggcacca	60
tgcagttct tctaactgcc tgtccatgca tgctcgccgc ttgtgttg tagcttctgt	120
ttccctggtg tctggtcgat cgatcgctcg cgcacggatt gtcttagtggt aggctctgg	180
ccctgcgcct acagtacgccc cacacatgga tcaaggccc tggtaaccct gttctgcagc	240
gacccaccgt gtcgatcatt aaccggccgg cgacactctg gctgttctgg aatctggatc	300
aattcgcctt cgccttcttg gagtaggtgc agatctgggt tggccttcgt ggacaggcgg	360
cggcgaagga gctatggaga tggccggcgc ggcggacagc cggggctgg cggcggcgc	420
gcccgaaccgg tacgagtcgc agaagcgccg ggactggcag acgttcgggc agtacctgc	480
caaccaccgg ccggccctgg agctggcccg gtgcagcggc ggcacgtgc tcgagttct	540
ccgctacctg gaccagttcg gcaagaccaa ggtgcacgcg cgggggtgcc ctttttcgg	600
ccacccgtcg cggccggcgc cgtgcccgtg cccgctcaag caggcgtggg gcagcctcga	660
cgcgctcgcc ggcggccctcc ggcggcccta tgaggagcac ggcggccggc ccgaggccaa	720

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cccccttcggg gcgcgcgccg tccggctcta cttccgcgag gtccgcgaca cccaggccaa	780
ggcgcgccggc atcgccatcg agaagaagcg ccgcaagcgc cacccgcggg cacacaggca	840
ggccaaggcag cagcaggacg ccggccagea gcagcagcag cactaccacc cccaccacca	900
ccaccaggcg tcgcccggcg cgccgcgggt gaccgagagt aggccgtgc tggctgacat	960
ggccgaaccc cgccgcgcgc acttccgtat cccgcacgcg cagtccctcc acggccactt	1020
cctgggtccg gtcaccgagc cgaccgaccc caccgcggg atggggggcg gggcacccgg	1080
cgaggacttg gtgctggcaa tggggccgcg cgccgaggcg cacgcgcgcg cggccgggtt	1140
cttgcgtccgc ctgtcccttc ttcaacttagct agcttgcgtt gtccactctc cgctgcctct	1200
atacgccat gggcaggat gcaaggctag gtaattaggc gtaatcaagc atgcaggttt	1260
tgctaatggc gatcgccctg atctctgcgc gccgtttggt cgtccatccg gctttggtg	1320
tttatgcgca gtcgtctccct ccgcgcgaca ttgcggcgcc cgcttgcaccc aaccgctgct	1380
gccttcgtt tgtatggggtt gtgcgtgggtt ttgtggacgc agtgcataaa tggctggatt	1440
agacggctct gtgtgtttt ctccatgact cggatctgt ggaaatttca tgtactacag	1500
ctgatctcaa tcgacttaac attttcctg gtt	1533

<210> SEQ_ID NO 141
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Panicum virgatum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1988960
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ_ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(133)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 141

Met Glu Met Ala Gly Ala Ala Asp Ser Pro Gly Leu Ala Ala Ala Arg			
1	5	10	15

Pro Asn Arg Tyr Glu Ser Gln Lys Arg Arg Asp Trp Gln Thr Phe Gly			
20	25	30	

Gln Tyr Leu Arg Asn His Arg Pro Pro Leu Glu Leu Ala Arg Cys Ser			
35	40	45	

Gly Ala His Val Leu Glu Phe Leu Arg Tyr Leu Asp Gln Phe Gly Lys			
50	55	60	

Thr Lys Val His Ala Pro Gly Cys Pro Phe Phe Gly His Pro Ser Pro			
65	70	75	80

Pro Ala Pro Cys Pro Cys Pro Leu Lys Gln Ala Trp Gly Ser Leu Asp			
85	90	95	

Ala Leu Val Gly Arg Leu Arg Ala Ala Tyr Glu Glu His Gly Gly Arg			
100	105	110	

Pro Glu Ala Asn Pro Phe Gly Ala Arg Ala Val Arg Leu Tyr Leu Arg			
115	120	125	

Glu Val Arg Asp Thr Gln Ala Lys Ala Arg Gly Ile Ala Tyr Glu Lys			
130	135	140	

Lys Arg Arg Lys Arg His Pro Pro Ala His Arg Gln Ala Lys Gln Gln			
145	150	155	160

Gln Asp Ala Gly Gln Gln Gln Gln His Tyr His Pro His His His	
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165	170	175
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His Gln Ala Ser Pro Ala Ala Ala Ala Val Thr Glu Ser Arg Arg Val 180	185	190
--	-----	-----

Leu Ala Asp Met Ala Glu Pro Pro Ala Pro His Phe Leu Ile Pro His 195	200	205
--	-----	-----

Ala Gln Phe Leu His Gly His Phe Leu Val Pro Val Thr Glu Pro Thr 210	215	220
--	-----	-----

Asp Pro Thr Ala Gly Met Gly Gly Gly Thr Gly Glu Asp Leu Val 225	230	235	240
--	-----	-----	-----

Leu Ala Met Ala Ala Ala Ala Glu Ala His Ala Ala Ala Ala Gly Phe 245	250	255
--	-----	-----

Leu Met Pro Leu Ser Phe Phe His 260
--

<210> SEQ_ID NO 142

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: *Medicago truncatula*

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Public GI ID no. 92891522

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (47) ..(179)

<223> OTHER INFORMATION: Pfam Name: DUF640

Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 142

Met Asn Ser Leu Gln Glu Phe Glu Ser Ser Thr Asn Asn Lys Asp Met 1	5	10	15
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Met Asn Thr Asn Pro Met Ile Asn Ile Thr Asn Pro Ser Ser Ser Met 20	25	30
---	----	----

Thr Met Thr Ile Pro Ser Ser Ser Thr Thr Ser Ala Ser Ser Ser Ser 35	40	45
---	----	----

Thr Ala Thr Thr Ser Pro Pro Ser Thr Thr Ser Thr Thr Pro Ser 50	55	60
---	----	----

Arg Tyr Glu Asn Gln Lys Arg Arg Asp Trp Asn Thr Phe Gly Gln Tyr 65	70	75	80
---	----	----	----

Leu Arg Asn His Arg Pro Pro Leu Ser Leu Ser Arg Cys Ser Gly Ala 85	90	95
---	----	----

His Val Leu Glu Phe Leu Arg Tyr Leu Asp Gln Phe Gly Lys Thr Lys 100	105	110
--	-----	-----

Val His Thr Leu Ile Cys Pro Phe Tyr Gly His Pro Asn Pro Pro Ala 115	120	125
--	-----	-----

Ser Cys Pro Cys Pro Leu Arg Gln Ala Trp Gly Ser Leu Asp Ala Leu 130	135	140
--	-----	-----

Ile Gly Arg Leu Arg Ala Ala Phe Glu Glu Asn Gly Gly Lys Pro Glu 145	150	155	160
--	-----	-----	-----

Ala Asn Pro Phe Gly Ala Arg Ala Val Arg Leu Tyr Leu Arg Glu Val 165	170	175
--	-----	-----

Arg Asp Ser Gln Ala Lys Ala Arg Gly Ile Ser Tyr Glu Lys Lys Lys 180	185	190
--	-----	-----

Arg Lys Arg Pro Pro Gln Pro Pro Pro Pro Pro Ser Asn Asn Ala 195	200	205
--	-----	-----

-continued

Thr Ile Thr Asp Leu His
210

```
<210> SEQ ID NO 143
<211> LENGTH: 828
<212> TYPE: DNA
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1073674
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 89
```

<400> SEQUENCE: 143

acacttttc tctcaatttc tctctttt	aaaacactaa tcactaaaat cttgattcac	60
tatatcgta aaaccaacgc taaatcaatt	aaactctctc aaagaaaaca agacaaagcc	120
ctactttga tggattcagg gtcacaacga	ccggggcctg ttagcgaagg cgatccgggt	180
ccgtccatcg taacccccc	ttcaccgcct gcgacgccta gcaggtacga gtcgcagaaa	240
cgacgtgact ggaccacgtt cttgcagttac	ctcaagaacc acaaggccgc ttttccctg	300
tcacggtgta gcgaggcaca tgccatcgag	ttcctcaagt acttagatca gttcggttaag	360
accaaagtcc acgtggcggc atgtccttac	tttggccatc agcaacccctc gtctccctgc	420
gtttgtcctc tcaagcaage ctgggggtct	ctcgatgccc tgatcggacg gttgagagca	480
gcctacgaag agaacgggtgg acggcccgag	tcgaaccctg tgcggcacg tgcggtagg	540
atttacttga gggaaagtca agaaaagtca	gccaaggccc gtgggagacc ctacgagaaa	600
aagaaaacgga aacggccaaac aactgttacc	accgtgagag ttgacgttgc ttctcgaga	660
caaagtgaag gagatggttg taacatcggt	gatccgtcgat atgtggccga ggctgtacct	720
ccttaattaa gttattatta ttgtcatgt	atattaaata cattatatat gtctggaact	780
cacatcacct tctttagtttta actattgaaa	atatttttgt tctagttc	828

```
<210> SEQ ID NO 144
<211> LENGTH: 799
<212> TYPE: DNA
<213> ORGANISM: Brassica napus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1118987
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 90
```

<400> SEQUENCE: 144

aaattctcgta ttgcgttata ttctcaaaac	caacgctaaa taaaaacact ctcaaagaaa	60
aacaaaaaaaaa aaaccctagt tttgatggaa	tcgactgatt cggggtcaca acaacatgga	120
ggtgaccccg gtccgtccctc cgtaacgccc	tcttcacctc cggcgacgcc gcctagcagg	180
tacgagtcgc aaaaacgacg tgactggAAC	acgttcttgc agtacctcaa gaaccacaag	240
ccgcctctcg cgttatcactg atgttagcgga	gcmcacgtga tcgagttcct caagtaccta	300
gatcagttcg gtaagaccaa agtccacgtg	gcmcacgtgcc cttacttgg acatcagcag	360
ctccctctc cttgcgttgc ttctctcaag	caagcctggg gatctctcgta tgctctgatc	420
ggacgggtga gagctgcgtA cgaggagcac	ggtggggaggc ctgattccaa cccttcgccc	480
gcacgtgcgg tcaggattta cttgagagaa	gtcagagaaa gtcaagccaa ggcacgtggg	540
atccatacg agaagaagaa acggaaacgg	gcaccaactg tcactaccgc tagaattgac	600

-continued

gttgctccgt cgagacaaaag tgaaggaggt ggtgggtgta acgacagtga tccgtctgtc	660
gccgaagctg taccgcctt aattaaatata ttatatcata ttaatttagtt ttcttgttat	720
attaaggcatg gaactcacac cttcgtaact ataatgtatt ttattttct atatgaacta	780
ttaagagttt tcttttgc	799

<210> SEQ ID NO 145
<211> LENGTH: 797
<212> TYPE: DNA
<213> ORGANISM: Parthenium argenta
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 1603237
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Encodes the peptide sequence at SEQ ID NO. 94
<400> SEQUENCE: 145

aacgaaataa accctaatac aacacccacc cactcaccca caaacatgtt aagcccaaca	60
tccctttcat cttcaatacg ctcacccgccc tcaacccgcca ccagtcgcct caaccgcgtac	120
gagagccaaa aacgcgggtga ctggaacaca ttccggtcgt tcctccgtaa ccacgaccca	180
cccttaaccc ttcccaactg caccagcaca cacgttatcg agttccctccg ttaccttgac	240
ccgtttggca aaactaaagt ccacacacat ctctgtccat ctttcggtca acccaaccct	300
ccccacactt gcccgtgccc cctccgtcag gcctggggca gcctcgatgc cctcattgg	360
cgtctccggg cagttttga agaaaacggg gggcagcccc agagtaaccc gtttggagct	420
agggctgtta ggttttattt acgtgaagtt aaggatgtc aagctaaagc tagaggatt	480
agttgtgaga agaagaggac gaagaaacgg ccacccgcccc ccactccgga tatttgg	540
gatcgctgat cgcggggcgtg ggtgaccctt tgctatcgat gatcgccggc gtgggtgacc	600
ttttgtataa ggggtgtacct ggggtgggtgg gcccgggtgt ttgacttaaa aaaaaaaaaag	660
ttacccgagt taatgggttataa tattttgtc tggttattaa atgggtataa agctatgtaa	720
tttgaatatt gaactcgata ttctgtttct tggaaatggg tagccataat tttgaagatc	780
attattgtta ttatctt	797

<210> SEQ ID NO 146
<211> LENGTH: 229
<212> TYPE: PRT
<213> ORGANISM: Glycine max
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres SEED LINE ME24507
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ceres CLONE ID no. 604111
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Functional Homolog of Ceres Clone ID no. 28780
at SEQ ID NO. 88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (28)..(160)
<223> OTHER INFORMATION: Pfam Name: DUF640
Pfam Description: Protein of unknown function (DUF640)

<400> SEQUENCE: 146

Met Ala Ser Ala Ser Gly Gly Ala Pro Pro Pro Gln Pro Thr Ser Thr			
1	5	10	15
Glu Ala Ala Pro Ala Ser Gly Ser Ser Ala Pro Ala Ile Ser Ala Ala			
20	25	30	

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Pro	Pro	Gln	Pro	Gly	Gly	Ser	Ser	Pro	Ala	Pro	Pro	Ser	Arg	Tyr	Glu
35				35					40				45		
Ser	Gln	Lys	Arg	Arg	Asp	Trp	Asn	Thr	Phe	Leu	Gln	Tyr	Leu	Gln	Asn
50		50			55			55		60					
His	Lys	Pro	Pro	Leu	Thr	Leu	Ala	Arg	Cys	Ser	Gly	Ala	His	Val	Ile
65					70			75				80			
Glu	Phe	Leu	Lys	Tyr	Leu	Asp	Gln	Phe	Gly	Lys	Thr	Lys	Val	His	Ile
	85					90			90			95			
Thr	Gly	Cys	Pro	Tyr	Tyr	Gly	Tyr	Pro	Asn	Pro	Pro	Ala	Pro	Cys	Ala
	100					105			105			110			
Cys	Pro	Leu	Lys	Gln	Ala	Trp	Gly	Ser	Leu	Asp	Ala	Leu	Ile	Gly	Arg
	115					120			120			125			
Leu	Arg	Ala	Ala	Tyr	Glu	Glu	Asn	Gly	Gly	Arg	Pro	Glu	Ser	Asn	Pro
	130					135			135			140			
Phe	Gly	Ala	Arg	Ala	Val	Arg	Ile	Tyr	Leu	Arg	Glu	Val	Arg	Glu	Gly
	145					150			150			155			160
Gln	Ala	Lys	Ala	Arg	Gly	Ile	Pro	Tyr	Glu	Lys	Lys	Arg	Lys	Arg	
	165					170			170			175			
Thr	Thr	Val	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Ser	Ser	Gly	Ala	
	180					185			185			190			
Val	Ala	Ser	Pro	Ser	Gly	Gly	Asp	Thr	Ala	Ile	Gly	Gly	Ala		
	195					200			200			205			
Gly	Ser	Ser	Ala	Ser	Leu	Thr	Ser	Ser	Ala	Thr	Ala	Thr	Ala	Asn	Asp
	210					215			215			220			
Thr	Thr	Thr	Thr	Val											
	225														

What is claimed is:

1. A method of modulating the low light tolerance of a plant, said method comprising introducing into a plant cell an exogenous nucleic acid comprising a nucleotide sequence encoding a polypeptide having 95% or greater sequence identity to SEQ ID NO: 112, wherein a plant produced from said plant cell exhibits a phenotypic difference relative to a corresponding control plant under low light conditions, wherein said phenotypic difference is a shortened hypocotyl. 35
2. A method of producing a plant, said method comprising growing a plant cell comprising an exogenous nucleic acid comprising a nucleotide sequence encoding a polypeptide having 95% or greater sequence identity to SEQ ID NO: 112, wherein said plant exhibits a phenotypic difference relative to a corresponding control plant under low light conditions, wherein said phenotypic difference is a shortened hypocotyl. 45
3. A plant comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a nucleotide sequence encoding a polypeptide having 95% or greater sequence identity to SEQ ID NO: 112, wherein said plant exhibits a phenotypic difference relative to a corresponding control plant under low light conditions, wherein said phenotypic difference is a shortened hypocotyl. 50
4. A plant comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a nucleotide sequence having 97% or greater sequence identity to SEQ ID NO: 111, wherein said plant exhibits a phenotypic difference relative to a corresponding control plant under low light conditions, wherein said phenotypic difference is a shortened hypocotyl. 55
5. The plant of claim 3, wherein said low light conditions comprise an irradiance of about 0.01 to about 20 $\mu\text{mol}/\text{m}^2/\text{s}$ of light. 60
6. The plant of claim 3, wherein said exogenous nucleic acid is operably linked to a regulatory region. 40
7. The plant of claim 3, wherein said regulatory region is a tissue-preferential, broadly expressing, or inducible promoter.
8. The plant of claim 3, wherein said plant is a dicot.
9. The plant of claim 8, wherein said plant is a member of the genus *Brassica*, *Glycine*, *Gossypium*, *Helianthus*, *Lactuca*, or *Medicago*.
10. The plant of claim 3, wherein said plant is a monocot. 45
11. The plant of claim 10, wherein said plant is a member of the genus *Cocos*, *Elaeis*, *Oryza*, *Panicum*, or *Zea*.
12. Progeny of the plant of claim 3, wherein said progeny comprises said exogenous nucleic acid, and wherein said progeny exhibits a phenotypic difference relative to a corresponding control plant under low light conditions. 50
13. Seed from the plant according to claim 3, said seed comprising said exogenous nucleic acid.
14. Vegetative tissue from the plant according to claim 3, said vegetative tissue comprising said exogenous nucleic acid. 55
15. Fruit from the plant according to claim 3, said fruit comprising said exogenous nucleic acid.
16. A food product comprising seed or vegetative tissue from the plant according to claim 3, said food product comprising said exogenous nucleic acid. 60
17. A feed product comprising seed or vegetative tissue from the plant according to claim 3, said feed product comprising said exogenous nucleic acid. 65

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